

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:08:42 ; Search time 18.855 Seconds
(without alignments)
171.264 Million cell updates/sec

Title: US-10-091-135-95
Perfect score: 420
Sequence: 1 NNYCKIKLGGVHTACKYK.....RGLTRGNPGPPAKNMKN 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New:
1: /SID55/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /SID55/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /SID55/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /SID55/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
5: /SID55/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /SID55/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /SID55/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /SID55/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	420	100.0	227	6	US-10-498-026-76
2	347.5	82.7	206	6	US-10-498-026-80
3	92	21.9	271	6	US-10-531-811-1
4	76.5	18.2	277	6	US-10-527-500-23
5	74.5	17.7	236	6	US-10-527-500-65
6	70	16.7	253	7	US-11-153-222A-2
7	70	16.7	298	7	US-11-124-367A-416
8	70	16.7	298	7	US-11-124-367A-417
9	70	16.7	298	7	US-11-124-367A-419
10	70	16.7	313	7	US-11-124-367A-418
11	70	16.7	416	7	US-11-124-367A-415
12	66.5	15.8	377	7	US-11-096-568A-2865
13	66.5	15.8	377	7	US-11-096-568A-2867
14	66.5	15.8	409	7	US-11-079-463-6373
15	66.5	15.8	500	7	US-11-096-568A-2864
16	65.5	15.6	2871	7	US-11-169-041-131
17	65.5	15.6	3002	6	US-10-821-234-916
18	65	15.5	737	7	US-11-152-366-28
19	64	15.2	135	7	US-11-188-298-3692
20	63	15.0	102	7	US-11-188-298-3770
21	62.5	14.9	332	7	US-11-188-298-3770
22	62.5	14.9	385	7	US-11-087-099-2354
23	62	14.8	254	7	US-11-172-740-2285
24	62	14.8	254	7	US-11-188-298-19953
25	62	14.8	423	7	US-11-087-099-5878

26	61	14.5	497	7	US-11-197-133A-16	Sequence 16, Appl
27	60	14.3	220	7	US-11-153-222A-3	Sequence 3, Appl1
28	59.5	14.2	201	6	US-10-467-557-5346	Sequence 5346, Ap
29	59.5	14.2	378	7	US-11-129-143-49	Sequence 49, Appl
30	59	14.0	253	7	US-11-172-740-561	Sequence 561, Appl
31	58.5	13.9	838	7	US-11-031-737A-11	Sequence 11, Appl
32	58.5	13.9	838	7	US-11-031-482-11	Sequence 11, Appl
33	58	13.8	1560	6	US-10-204-639-63	Sequence 63, Appl
34	58	13.8	2911	7	US-11-090-817-706	Sequence 706, Appl
35	57.5	13.7	176	7	US-11-096-568A-1297	Sequence 1297, Ap
36	57.5	13.7	202	7	US-11-096-568A-1296	Sequence 1296, Ap
37	57.5	13.7	206	6	US-10-467-657-7716	Sequence 7716, Ap
38	57.5	13.7	443	7	US-11-172-740-528	Sequence 528, App
39	57.5	13.7	519	7	US-11-033-039-442	Sequence 442, App
40	57	13.6	231	6	US-10-821-234-943	Sequence 943, App
41	56.5	13.5	249	7	US-11-096-568A-33644	Sequence 33644, A
42	56.5	13.5	283	7	US-11-096-568A-33643	Sequence 33643, A
43	56.5	13.5	287	7	US-11-096-568A-33642	Sequence 33642, A
44	56.5	13.5	359	7	US-11-108-528-62	Sequence 62, Appl
45	56.5	13.5	453	7	US-11-096-568A-6095	Sequence 6095, Ap

ALIGNMENTS

RESULT 1
US-10-498-026-76
; Sequence 76, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498.026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 76
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-76

Query Match 100.0%; Score 420; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 4.7e-42;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	NNYCKIKLGGVHTACKYKSLKPCNCKGVVSYGLTKQEKQDILKEHNDPROKIARGL	60
Db	24	NNYCKIKLGGVHTACKYKSLKPCNCKGVVSYGLTKQEKQDILKEHNDPROKIARGL	83
Qy	61	TRGNPGPPAKNMKN 76	
Db	84	TRGNPGPPAKNMKN 99	

RESULT 2
US-10-498-026-80
; Sequence 80, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498.026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 80
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-80

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; SEQ ID NO 162
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Vesputa flavopilosa (Yellow jacket) (Wasp)
US-09-847-208-162

Query Match      100.0%; Score 420; DB 3; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKCLKGGVHTACKYGLSKPNCNGKVVVSYGLTKQEKODILKEHNDFRQKIARGLE 60
   |||||
DB 1 NNYCKIKCLKGGVHTACKYGLSKPNCNGKVVVSYGLTKQEKODILKEHNDFRQKIARGLE 60
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QY 61 TRGNPGPQPPAKNMKN 76
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DB 61 TRGNPGPQPPAKNMKN 76
   |||||

RESULT 3
US-10-091-135-16
; Sequence 16, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Vesputa vulgaris
US-10-091-135-16

Query Match      100.0%; Score 420; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKCLKGGVHTACKYGLSKPNCNGKVVVSYGLTKQEKODILKEHNDFRQKIARGLE 60
   |||||
DB 1 NNYCKIKCLKGGVHTACKYGLSKPNCNGKVVVSYGLTKQEKODILKEHNDFRQKIARGLE 60
   |||||

QY 61 TRGNPGPQPPAKNMKN 76
   |||||
DB 61 TRGNPGPQPPAKNMKN 76
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RESULT 4
US-10-091-135-64
; Sequence 64, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 64
; LENGTH: 204
; TYPE: PRT
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; ORGANISM: Vesputa vulgaris
US-10-091-135-64

Query Match      100.0%; Score 420; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKCLKGGVHTACKYGLSKPNCNGKVVVSYGLTKQEKODILKEHNDFRQKIARGLE 60
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DB 1 NNYCKIKCLKGGVHTACKYGLSKPNCNGKVVVSYGLTKQEKODILKEHNDFRQKIARGLE 60
   |||||

QY 61 TRGNPGPQPPAKNMKN 76
   |||||
DB 61 TRGNPGPQPPAKNMKN 76
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RESULT 5
US-10-091-135-65
; Sequence 65, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 65
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Vesputa flavopilosa
US-10-091-135-65

Query Match      100.0%; Score 420; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.6e-41;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKCLKGGVHTACKYGLSKPNCNGKVVVSYGLTKQEKODILKEHNDFRQKIARGLE 60
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DB 1 NNYCKIKCLKGGVHTACKYGLSKPNCNGKVVVSYGLTKQEKODILKEHNDFRQKIARGLE 60
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QY 61 TRGNPGPQPPAKNMKN 76
   |||||
DB 61 TRGNPGPQPPAKNMKN 76
   |||||

RESULT 6
US-10-091-135-81
; Sequence 81, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 81
; LENGTH: 204
; TYPE: PRT
; ORGANISM: Vesputa vulgaris
US-10-091-135-81
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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2006, 11:05:57 ; Search time 116.321 Seconds
(without alignments)
272.996 Million cell updates/sec

Title: US-10-091-135-95

Perfect score: 420

Sequence: 1 NNYCKIKLKGCVHTACKYK.....RGLTRGNPGQPAPKMNKN 76

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA Main:

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	420	100.0	76	4	US-10-091-135-95
2	420	100.0	204	3	US-09-847-208-162
3	420	100.0	204	4	US-10-091-135-16
4	420	100.0	204	4	US-10-091-135-64
5	420	100.0	204	4	US-10-091-135-65
6	420	100.0	204	4	US-10-091-135-81
7	420	100.0	204	4	US-10-719-553-39
8	420	100.0	209	3	US-09-957-806A-22
9	420	100.0	210	4	US-10-001-245-214
10	420	100.0	227	3	US-09-847-208-170
11	420	100.0	227	5	US-10-809-689-82
12	416	99.0	204	3	US-09-847-208-166
13	416	99.0	204	4	US-10-091-135-66
14	414	98.6	204	3	US-09-847-208-165
15	414	98.6	204	4	US-10-091-135-63
16	397	94.5	204	3	US-09-847-208-163
17	397	94.5	204	4	US-10-091-135-67
18	393.5	93.7	201	4	US-10-001-245-119
19	393.5	93.7	202	4	US-10-001-245-117
20	393.5	93.7	203	4	US-10-001-245-118
21	379	90.2	194	4	US-10-001-245-120
22	373	88.8	198	4	US-10-001-245-121
23	347.5	82.7	206	3	US-09-847-208-171
24	347.5	82.7	206	4	US-10-091-135-68
25	347.5	82.7	206	5	US-10-809-689-86
26	345.5	82.3	205	3	US-09-847-208-167
27	345.5	82.3	205	4	US-10-091-135-69

28	341.5	81.3	192	4	US-10-001-245-122	Sequence 122, Appl
29	313	74.5	157	4	US-10-091-135-94	Sequence 94, Appl
30	306	72.9	202	3	US-09-847-208-160	Sequence 160, Appl
31	306	72.9	202	3	US-09-847-208-161	Sequence 161, Appl
32	306	72.9	202	4	US-10-091-135-74	Sequence 74, Appl
33	306	72.9	202	4	US-10-091-135-75	Sequence 75, Appl
34	305	72.6	204	4	US-10-091-135-70	Sequence 70, Appl
35	305	72.6	227	3	US-09-847-208-90	Sequence 90, Appl
36	296.5	70.6	203	3	US-09-847-208-86	Sequence 86, Appl
37	296.5	70.6	203	4	US-10-091-135-71	Sequence 71, Appl
38	295	70.2	202	3	US-09-847-208-172	Sequence 172, Appl
39	295	70.2	202	4	US-10-091-135-73	Sequence 73, Appl
40	293	69.8	166	4	US-10-001-245-124	Sequence 124, Appl
41	287	68.3	205	4	US-10-091-135-72	Sequence 72, Appl
42	287	68.3	215	3	US-09-847-208-91	Sequence 91, Appl
43	281	66.9	170	4	US-10-001-245-123	Sequence 123, Appl
44	279	66.4	50	4	US-10-091-135-93	Sequence 93, Appl
45	260	61.9	206	3	US-09-847-208-150	Sequence 150, Appl

ALIGNMENTS

RESULT 1

US-10-091-135-95
; Sequence 95, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; FILE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 95
; LENGTH: 76
; TYPE: PRT
; ORGANISM: *Vesputia vulgaris*
US-10-091-135-95

Query Match		100.0%	Score 420;	DB 4;	Length 76;
Best Local Similarity		100.0%	Pred. No. 4.9e-42;		
Matches		76;	Conservative	0;	Mismatches 0;
				Indels	0; Gaps 0;
QY	1	NNYCKIKLKGCVHTACKYKSLKPNCGNKVVSYGLTKQEKQDILKEHNDFRQKIARGLE	60		
Db	1	NNYCKIKLKGCVHTACKYKSLKPNCGNKVVSYGLTKQEKQDILKEHNDFRQKIARGLE	60		
QY	61	TRGNPGQPAPKMNKN	76		
Db	61	TRGNPGQPAPKMNKN	76		

RESULT 2

US-09-847-208-162
; Sequence 162, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daoceng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; FILE OF INVENTION: IGE-MEDIATED ALLERGIC DISEASES
; FILE REFERENCE: UC67.002A
; CURRENT APPLICATION NUMBER: US/09/847,208
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0


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DB 1 NNYCKIKLKGVTACKYGLKPNCGNKVVSYGLTKQEKODILKEHNDFRQKIARGLE 60
OY 61 TRGNPGQPAPKMKN 76
DB 61 TRGNPGQPAPKMKN 76

RESULT 2
US-08-614-935-2
; Sequence 2, Application US/08614935
; Patent No. 5804201
; GENERAL INFORMATION:
; APPLICANT: King, Te P.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 11-MAR-1996
; CLASSIFICATION: 436
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-156
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Vesputula vulgaris
US-08-614-935-2

Query Match 100.0%; Score 420; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 5e-40;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NNYCKIKLKGVTACKYGLKPNCGNKVVSYGLTKQEKODILKEHNDFRQKIARGLE 60
DB 1 NNYCKIKLKGVTACKYGLKPNCGNKVVSYGLTKQEKODILKEHNDFRQKIARGLE 60
OY 61 TRGNPGQPAPKMKN 76
DB 61 TRGNPGQPAPKMKN 76

RESULT 3
US-09-130-287-2
; Sequence 2, Application US/09130287
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; Patent No. 6106844
; GENERAL INFORMATION:
; APPLICANT: King, Te P.
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
; NUMBER OF SEQUENCES: 81
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: David A. Jackson, Esq.
; STREET: 411 Hackensack Ave, Continental Plaza, 4th
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION NUMBER: US 08/614,935
; APPLICATION NUMBER: 11-MAR-1996
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-156 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201-487-5800
; TELEFAX: 201-343-1684
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE:
; ORIGINAL SOURCE:
; ORGANISM: Vesputula vulgaris
US-09-130-287-2

Query Match 100.0%; Score 420; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 5e-40;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NNYCKIKLKGVTACKYGLKPNCGNKVVSYGLTKQEKODILKEHNDFRQKIARGLE 60
DB 1 NNYCKIKLKGVTACKYGLKPNCGNKVVSYGLTKQEKODILKEHNDFRQKIARGLE 60
OY 61 TRGNPGQPAPKMKN 76
DB 61 TRGNPGQPAPKMKN 76

RESULT 4
US-09-541-759-6
; Sequence 6, Application US/09541759
; Patent No. 6723322
; GENERAL INFORMATION:
; APPLICANT: Lustigman, Sara
; APPLICANT: Pearlmann, Eric
; APPLICANT: Unnasch, Thomas
; TITLE OF INVENTION: ANGIOGENIC ONCHOCERCA VOLVULUS PROTEINS AND USES THEREOF
; FILE REFERENCE: 63475/252
; CURRENT APPLICATION NUMBER: US/09/541,759
; CURRENT FILING DATE: 2000-04-03
```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:57:41 ; Search time 22.916 Seconds
(without alignments)
274.190 Million cell updates/sec

Title: US-10-091-135-95
Perfect score: 420
Sequence: 1 NNYCKIKLKGVTACKYG.....RGLETRGNPGPPAKNNKN 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/H COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	420	100.0	204	1	US-08-419-414-9 Sequence 9, Appli
2	420	100.0	204	1	US-08-614-935-2 Sequence 2, Appli
3	420	100.0	204	2	US-09-130-287-2 Sequence 2, Appli
4	420	100.0	227	2	US-09-541-759-6 Sequence 6, Appli
5	414	98.6	204	1	US-08-614-935-1 Sequence 1, Appli
6	414	98.6	204	2	US-09-130-287-1 Sequence 5, Appli
7	305	72.6	204	1	US-08-614-935-5 Sequence 5, Appli
8	305	72.6	204	2	US-09-130-287-5 Sequence 8, Appli
9	296.5	70.6	203	1	US-08-419-414-8 Sequence 3, Appli
10	296.5	70.6	203	1	US-08-614-935-3 Sequence 3, Appli
11	296.5	70.6	203	2	US-09-130-287-3 Sequence 4, Appli
12	289	68.8	205	1	US-08-614-935-4 Sequence 4, Appli
13	289	68.8	205	2	US-09-130-287-4 Sequence 10, Appli
14	243	57.9	205	1	US-08-419-414-10 Sequence 6, Appli
15	243	57.9	205	1	US-08-614-935-6 Sequence 7, Appli
16	243	57.9	205	1	US-08-614-935-7 Sequence 7, Appli
17	243	57.9	205	2	US-09-130-287-7 Sequence 7, Appli
18	243	57.9	205	2	US-09-130-287-6 Sequence 46, Appli
19	180	42.9	31	1	US-08-614-935-46 Sequence 46, Appli
20	180	42.9	31	2	US-09-130-287-46 Sequence 45, Appli
21	174	41.4	31	1	US-08-614-935-45 Sequence 45, Appli
22	174	41.4	31	2	US-09-130-287-45 Sequence 53, Appli
23	168	40.0	31	1	US-08-614-935-53 Sequence 54, Appli
24	168	40.0	31	2	US-08-614-935-54 Sequence 54, Appli
25	168	40.0	31	2	US-09-130-287-53 Sequence 54, Appli
26	168	40.0	31	2	US-09-130-287-54 Sequence 30, Appli
27	160	38.1	166	1	US-08-614-935-30 Sequence 30, Appli

Query Match 100.0%; Score 420; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 5e-40;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Sequence 30, Appli
Sequence 55, Appli
Sequence 55, Appli
Sequence 57, Appli
Sequence 56, Appli
Sequence 56, Appli
Sequence 43, Appli
Sequence 43, Appli
Sequence 48, Appli
Sequence 58, Appli
Sequence 58, Appli
Sequence 58, Appli
Sequence 59, Appli
Sequence 49, Appli
Sequence 49, Appli
Sequence 42, Appli

ALIGNMENTS

RESULT 1
US-08-419-414-9
; Sequence 9, Application US/08419414
; Patent No. 5753787
; GENERAL INFORMATION:
; APPLICANT: Hawdon, John M.
; APPLICANT: Hotez, Peter J.
; APPLICANT: Jones, Brian F.
; TITLE OF INVENTION: Hookworm Vaccine
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,414
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Vespula vulgaris
; US-08-419-414-9

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Best Local Similarity 100.0%; Pred. No. 4.5e-38;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKCLKGGVHTACKYGLSKPNCNKGKVVVSYGLTKQEKDILKEHNDPROKIARGLE 60
DB 1 NNYCKIKCLKGGVHTACKYGLSKPNCNKGKVVVSYGLTKQEKDILKEHNDPROKIARGLE 60
QY 61 TRGNPGPOPPAKNMKN 76
DB 61 TRGNPGPOPPAKNMKN 76

RESULT 2
ID - VAS VESVU STANDARD; PRT; 227 AA.
AC Q05I10; Q0UB91;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Venom allergen 5 precursor (Antigen 5) (Ag5) (Allergen Ves v 5) (Ves v
V).
OS Vesputa vulgaris (Yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidiae; Vespinae; Vespula.
OX NCBI_TaxID=7454;
RN (1) _
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=93203603; PubMed=8454859;
RA Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
RT "Sequence analysis and antigenic cross-reactivity of a venom allergen,
RT antigen 5, from hornets, wasps, and yellow jackets.";
RL J. Immunol. 150:2823-2830(1993).
RN (2)
RP NUCLEOTIDE SEQUENCE OF 24-227.
RA Suck R., Hagen S., Fiebig H.;
RT "Molecular cloning of a genomic sequence from the venom allergen
RT antigen 5 from Vespula vulgaris.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the CRISP family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR EMBL; M98858; AAA30333.1; -; mRNA.
DR EMBL; AJ238849; CAB42887.1; -; Genomic_DNA.
DR PDB; 1QNX; X-ray; A=24-227.
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR InterPro; IPR002413; V5_allergen.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00838; V5TPXLKE.
DR PRINTS; PR00837; V5TPXLKE.
DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; CRISP_1; 1.
DR PROSITE; PS01010; CRISP_2; 1.
KW 3D-structure; Allergen; Direct protein sequencing; Signal.
FT SIGNAL 1 23
FT CHAIN 24 227 Venom allergen 5.
FT DISULFID 27 40 By similarity.
FT DISULFID 31 124 By similarity.
FT DISULFID 49 117 By similarity.
FT DISULFID 193 210 By similarity.
FT DISULFID 109 109 V -> I (in Ref. 2).
FT CONFLICT 118 118 Q -> E (in Ref. 2).
FT CONFLICT 173 173 D -> N (in Ref. 2).
FT CONFLICT 219 219 M -> K (in Ref. 2).
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FT HELIX 26 28
FT TURN 32 33
FT HELIX 38 41
FT STRAND 53 57
FT HELIX 61 79
FT TURN 80 81
FT TURN 87 88
FT STRAND 94 94
FT STRAND 101 102
FT HELIX 104 114
FT TURN 115 116
FT STRAND 133 141
FT HELIX 149 157
FT HELIX 158 162
FT TURN 169 171
FT HELIX 174 183
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FT STRAND 190 200
FT TURN 201 202
FT STRAND 203 213
FT TURN 219 220
FT STRAND 226 227
SQ SEQUENCE 227 AA; 25798 MW; 99E9813740A66F55 CRC64;

Query Match 100.0%; Score 420; DB 1; Length 227;
Best Local Similarity 100.0%; Pred. No. 5.1e-38;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKCLKGGVHTACKYGLSKPNCNKGKVVVSYGLTKQEKDILKEHNDPROKIARGLE 60
DB 24 NNYCKIKCLKGGVHTACKYGLSKPNCNKGKVVVSYGLTKQEKDILKEHNDPROKIARGLE 83
QY 61 TRGNPGPOPPAKNMKN 76
DB 84 TRGNPGPOPPAKNMKN 99

RESULT 3
ID - VAS VESPE STANDARD; PRT; 204 AA.
AC P35785;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves p 5) (Ves p V).
OS Vesputa pensylvanica (Western yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidiae; Vespinae; Vespula.
OX NCBI_TaxID=30213;
RN (1) _
RP PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94044316; PubMed=8227862;
RA Hoffman D.R.;
RT "Allergens in Hymenoptera venom. XXV: the amino acid sequences of
RT antigen 5 molecules and the structural basis of antigenic cross-
RT reactivity.";
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the CRISP family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; C44583; C44583.
DR HSP; Q05110; 1QNX.
```

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:53:37 ; Search time 112.26 Seconds
(without alignments)
477.644 Million cell updates/sec

Title: US-10-091-135-95
Perfect score: 420
Sequence: 1 NNYCKIKLKGHVHTACKY.....RGLTRGNPGQPAPKXMKXN 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_05.80: *
1: uniprot_sprot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	420	100.0	207	1 VA5_VESFL	P35783 vespula fla
2	420	100.0	224	1 VA5_VESVU	Q05110 vespula vul
3	416	99.0	204	1 VA5_VESPE	P35785 vespula pen
4	414	98.6	204	1 VA5_VESMC	P35760 vespula mac
5	397	94.5	204	1 VA5_VESGE	P35784 vespula ger
6	347.5	82.7	206	1 VA5_VESVI	P35787 vespula vid
7	345.5	82.3	205	1 VA5_VESSQ	P35786 vespula equ
8	306	72.9	202	1 VA51_VESCR	P35781 vespa crabr
9	306	72.9	202	1 VA52_VESCR	P35782 vespa crabr
10	305	72.6	227	1 VA52_DOLMA	P10736 dolichovesp
11	296.5	70.6	203	1 VA5_DOLAR	Q05108 dolichovesp
12	295	70.2	202	1 VA5_VESMA	P81657 vespa manda
13	287	68.3	215	1 VA53_SOLMA	P10737 dolichovesp
14	262	62.4	206	1 VA5_FOLGA	P83377 polistes ga
15	260	61.9	206	1 VA5_FOLDO	P81656 polistes do
16	260	61.9	227	2 Q68KJ8_FOLDO	Q68KJ8 polistes do
17	250	59.5	205	1 VA5_POLFU	P35780 polistes fu
18	243	57.9	205	1 VA5_POLEX	P35759 polistes ex
19	243	57.9	209	1 VA5_POLAN	Q05109 polistes an
20	240	57.1	226	2 Q68KJ9_POLEX	Q68KJ9 polistes ex
21	231.5	55.1	207	1 VA5_POFSR	Q72156 polybia scu
22	156	37.1	211	1 VA3_SOIRI	P35779 solenopsis
23	156	37.1	234	1 VA3_SOLIN	P35778 solenopsis
24	92	21.9	271	2 Q9XZ44_LUTLO	Q9XZ44 lutomyia l
25	91	21.7	392	2 Q9VFY2_DROME	Q9VFY2 drosophila
26	89	21.2	424	2 Q9XZ41_ANCCA	Q9XZ41 ancylostoma
27	88	21.0	122	2 O44205_MEGSC	O44205 megaselia s
28	88	21.0	135	2 O44206_MEGSC	O44206 megaselia s
29	88	21.0	424	2 Q76744_NECAM	Q76744 necator ame
30	87.5	20.8	255	2 Q8T9W0_AEDAE	Q8T9W0 aedes aegypt
31	86.5	20.6	255	2 Q5MIV5_AEDAL	Q5MIV5 aedes albop

32	86	20.5	424	1 ASP_ANCCA	Q16937 ancylostoma
33	84.5	20.1	248	2 Q9BIQ6_9BILA	Q9BIQ6 cooperia pu
34	84.5	20.1	248	2 Q9BIQ8_9BILA	Q9BIQ8 cooperia pu
35	84	20.0	425	2 Q816X0_9BILA	Q816X0 ancylostoma
36	83.5	19.9	217	2 Q7ZIH2_9BILA	Q7ZIH2 ancylostoma
37	82.5	19.6	459	2 Q45132_HAECCO	Q45132 haemonchus
38	80.5	19.2	253	2 Q7PRE8_ANOGA	Q7PRE8 anopheles g
39	80.5	19.2	260	2 Q7PGC9_ANOGA	Q7PGC9 anopheles g
40	80.5	19.2	491	2 Q9BIQ4_9BILA	Q9BIQ4 cooperia pu
41	80	19.0	425	2 Q77153_9BILA	Q77153 ancylostoma
42	79	18.8	256	2 Q5MIT3_AEDAL	Q5MIT3 aedes albop
43	78.5	18.7	113	2 Q4QQ77_DROME	Q4QQ77 drosophila
44	78.5	18.7	263	2 Q8ML52_DROME	Q8ML52 drosophila
45	78.5	18.7	307	2 Q7RA91_PLAYO	Q7RA91 plasmodium

ALIGNMENTS

RESULT 1
VAS_VESFL
ID - VAS_VESFL STANDARD; PRT; 204 AA.
AC P35783;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves f 5) (Ves f V).
OS Vespula flavopilosa (Yellow Jacket) (Waep).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidae;
OC Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=30211;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94044316; PubMed=8227862;
RA Hofman D.R.;
RT "Allergens in Hymenoptera venom. XXV: the amino acid sequences of
RT antigen 5 molecules and the structural basis of antigenic cross-
RT reactivity.";
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -!- FUNCTION: May have an ancestral function in the promotion of ovum
CC -!- fertilization by sperm.
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the CRISP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A44583; A44583.
CC HSSP; Q05110; IQNX.
CC SMR; P35783; 1-204.
CC InterPro; IPR002413; Allrgn_V5/Tpx1.
CC InterPro; IPR002413; V5_allergen.
CC Pfam; PF00188; SCP; 1.
CC PRINTS; PR00838; VSALLERGEN.
CC PRINTS; PR00837; V5TPXLIKE.
CC ProDom; PD000542; Allrgn_V5/Tpx1; 1.
CC SMART; SM00198; SCP; 1.
CC PROSITE; PS01009; CRISP_1; 1.
CC PROSITE; PS01010; CRISP_2; 1.
KW Allergen; Direct protein sequencing.
FT DISULFID 4 17 By similarity.
FT DISULFID 8 101 By similarity.
FT DISULFID 26 94 By similarity.
FT DISULFID 170 187 By similarity.
SQ SEQUENCE 204 AA; 23274 MW; 7667232536AB2FC5 CRC64;
Query Match 100.0%; Score 420; DB 1; Length 204;

Db 1 NNYCKIKCLGGVHTACKYGLKPCNGKKNVVSGLTKQEKQDILKEHNDPRQKIARGLE 60
Qy 61 TRGNPGPPPPAKNMKN 76
Db 61 TRGNPGPPPPAKNMKN 76

RESULT 3

B37329
antigen 5 - eastern yellowjacket
C:Species: Vespa maculifrons (eastern yellowjacket)
C:Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C:Accession: B37329
R:Lu, G.; Villalba, M.; Coscia, M.R.; Hoffman, D.R.; King, T.P.
submitted to the Protein Sequence Database, August 1992
A:Reference number: A37329
A:Accession: B37329
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <LUI>
A:Cross-references: UNIPROT:P35760; UNIPARC:UPI0000138092
C:Superfamily: yellowjacket venom allergen antigen.5

Query Match 98.6%; Score 414; DB 2; Length 204;
Best Local Similarity 98.7%; Pred. No. 4.5e-37;
Matches 75; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NNYCKIKCLGGVHTACKYGLKPCNGKKNVVSGLTKQEKQDILKEHNDPRQKIARGLE 60
Db 1 NNYCKIKCLGGVHTACKYGLKPCNGKKNVVSGLTKQEKQDILKEHNDPRQKIARGLE 60
Qy 61 TRGNPGPPPPAKNMKN 76
Db 61 TRGNPGPPPPAKNMKN 76

RESULT 4

B44583
venom allergen antigen Ves g 5 - German yellowjacket
C:Species: Vespa germanica (German yellowjacket)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: B44583; A44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: B44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
A:Cross-references: UNIPROT:P35784; UNIPARC:UPI0000138090
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 94.5%; Score 397; DB 2; Length 204;
Best Local Similarity 94.7%; Pred. No. 3e-35;
Matches 72; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NNYCKIKCLGGVHTACKYGLKPCNGKKNVVSGLTKQEKQDILKEHNDPRQKIARGLE 60
Db 1 NNYCKIKCLGGVHTACKYGLKPCNGKKNVVSGLTKQEKQDILKEHNDPRQKIARGLE 60
Qy 61 TRGNPGPPPPAKNMKN 76
Db 61 TRGNPGPPPPAKNMKN 76

RESULT 5

B44583
venom allergen antigen Ves vi 5 - yellowjacket (Vespa vidua)
C:Species: Vespa vidua
C:Date: 27-Jun-1994, #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: B44583; E44522

R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: B44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-206 <HOF>
A:Cross-references: UNIPROT:P35787; UNIPARC:UPI0000138095
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 82.7%; Score 347.5; DB 2; Length 206;
Best Local Similarity 82.9%; Pred. No. 6.3e-30;
Matches 63; Conservative 5; Mismatches 7; Indels 1; Gaps 1;

Qy 2 NYCKIKCLGGVHTACKYGLKPCNGKKNVVSGLTKQEKQDILKEHNDPRQKIARGLE 60
Db 3 NYCKIKCLGGVHTACKYGLKPCNGKKNVVSGLTKQEKQDILKEHNDPRQKIARGLE 62
Qy 61 TRGNPGPPPPAKNMKN 76
Db 63 TRGNPGPPPPAKNMKN 78

RESULT 6

D44583
venom allergen antigen Ves s 5 - southern yellowjacket
C:Species: Vespa squamosa (southern yellowjacket)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: D44583; D4522
R:Hoffman, D.R.

J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: D44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-205 <HOF>
A:Cross-references: UNIPROT:P35786; UNIPARC:UPI0000138094
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 82.3%; Score 345.5; DB 2; Length 205;
Best Local Similarity 82.9%; Pred. No. 1e-29; 7; Indels 1; Gaps 1;

Qy 2 NYCKIKCLGGVHTACKYGLKPCNGKKNVVSGLTKQEKQDILKEHNDPRQKIARGLE 60
Db 2 DYCKIKCLGGVHTACKYGLKPCNGKKNVVSGLTKQEKQDILKEHNDPRQKIARGLE 61
Qy 61 TRGNPGPPPPAKNMKN 76
Db 62 TRGNPGPPPPAKNMKN 77

RESULT 7

H44583
venom allergen antigen Vesp c 5.02 - European hornet
C:Species: Vespa crabro (European hornet)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: H44583; H4522
R:Hoffman, D.R.

J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: H44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-202 <HOF>

A:Cross-references: UNIPROT:P35782; UNIPARC:UPI0000138080
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 72.9%; Score 306; DB 2; Length 202;
Best Local Similarity 74.7%; Pred. No. 1.8e-25;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:56:21 ; Search time 15.9542 Seconds
(without alignments)
458.342 Million cell updates/sec

Title: US-10-091-135-95
Perfect score: 420
Sequence: 1 NNYCKIKCLRGVHTACKYG.....RGLTRNGPGPPAKNMKN 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	420	100.0	204	2 A44583	venom allergen ant
2	416	99.0	204	2 A44583	venom allergen ant
3	414	98.6	204	2 B37329	antigen 5 - easter
4	397	94.5	204	2 A44583	venom allergen ant
5	347.5	82.7	206	2 E44583	venom allergen ant
6	345.5	82.3	205	2 D44583	venom allergen ant
7	306	72.9	202	2 H44583	venom allergen ant
8	306	72.9	202	2 G44583	venom allergen ant
9	305	72.6	227	2 A31085	antigen 5-2 precu
10	289	68.8	213	2 B31085	antigen 5-3 precu
11	250	59.5	205	2 F44583	venom allergen ant
12	243	57.9	205	2 A37329	antigen 5 - paper
13	156	37.1	211	2 B58853	venom allergen Sol
14	156	37.1	212	2 B37330	venom allergen III
15	75	17.9	202	2 AE1278	phosphoribosyl ant
16	74	17.6	737	1 KIMSC	protein kinase C (
17	74	17.6	737	1 KIMTCE	protein kinase C (
18	73	17.4	385	2 T21763	hypothetical prote
19	70.5	16.8	2500	2 G71609	hypothetical prote
20	69.5	16.5	401	2 G96972	hypothetical prote
21	69	16.4	434	2 AE1326	hypothetical prote
22	68	16.2	605	2 F71724	aspartate-tRNA lig
23	67	15.0	2025	2 D86201	protein F12K11.6 [
24	65.5	15.6	1295	2 A32901	glpi protein precu
25	65.5	15.6	2871	2 A55567	fibrillin I - bovi
26	65.5	15.6	2871	2 A55624	fibrillin-1 precu
27	65.5	15.6	3002	2 A47221	fibrillin 1 precu
28	65	15.5	615	2 C97723	aspartate-tRNA lig
29	65	15.5	737	1 S28942	protein kinase C (

hypothetical prote
hypothetical prote
protein phosphatas
MADS box protein A
conserved hypotbet
protein kinase C (

30 64.5 15.4 196 2 T27833
31 64.5 15.4 246 2 T24493
32 64.5 15.4 658 2 S68418
33 64 15.2 251 2 T00556
34 64 15.2 380 1 G64509
35 64 15.2 736 1 KIRBCE
36 63.5 15.1 292 2 H81857
37 63.5 15.1 342 2 B81086
38 63.5 15.1 453 1 A25326
39 63 15.0 327 2 A83425
40 62.5 14.9 385 2 D72211
41 62.5 14.9 517 1 S19243
42 62 14.8 254 2 T10467
43 62 14.8 396 2 B42214
44 62 14.8 423 2 T50923
45 62 14.8 430 2 C70176

hypothetical prote
hypothetical prote
MADS box protein D
acetylornithine tr
probable ATP-depen

ALIGNMENTS

RESULT 1

A44583
venom allergen antigen Ves f 5 - yellowjacket (Vespula flavopilosa)
C:Species: Vespula flavopilosa
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A44583; B44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mol
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: A44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
A:Cross-references: UNIPROT:P35783; UNIPARC:UPI000013808F
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 100.0%; Score 420; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1e-37;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKCLRGVHTACKYGLKPCNGKNKVVSGLTKQEKQDILKEHNDFRQKIARGLE 60
DB 1 NNYCKIKCLRGVHTACKYGLKPCNGKNKVVSGLTKQEKQDILKEHNDFRQKIARGLE 60
QY 61 TRGNPGPOPAPAKNMKN 76
DB 61 TRGNPGPOPAPAKNMKN 76

RESULT 2

A44583
venom allergen antigen Ves p 5 - western yellowjacket
C:Species: Vespula pensylvanica (western yellowjacket)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: C44583; C44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mol
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: C44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
A:Cross-references: UNIPROT:P35785; UNIPARC:UPI0000138093
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 99.0%; Score 416; DB 2; Length 204;
Best Local Similarity 97.4%; Pred. No. 2.7e-37;
Matches 74; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKCLRGVHTACKYGLKPCNGKNKVVSGLTKQEKQDILKEHNDFRQKIARGLE 60

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XX SQ Sequence 76 AA;
Query Match 100.0%; Score 420; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 5.7e-45;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVVSYGLTKQEKQDILKEHNDFRQKIARGLE 60

QY 61 TRGNPGPPPAKNNKN 76
DB 61 TRGNPGPPPAKNNKN 76

RESULT 2
AAW35688
ID AAW35688 standard; peptide; 204 AA.
XX
AC AAW35688;
XX
DT 13-MAY-1998 (first entry)
XX
DE Vespid antigen 5s from Vesputa vulgaris (yellowjacket).
XX
KW Immunomodulatory peptide; vespid antigen 5; immunogenic; allergy;
KW vespid venom; white face hornet wasp; immunodominant peptide; T cell.
XX
OS Vesputa vulgaris.
XX
PN WO9733910-A1.
XX
PD 18-SEP-1997.
XX
PF 11-MAR-1997; 97WO-US003753.
XX
PR 11-MAR-1996; 96US-00614935.
XX
PA (UYRQ) UNIV ROCKEFELLER.
XX
PI King TP;
XX
DR WPI; 1997-470817/43.
XX
PT Vespid venom antigen 5 peptide fragments - useful to treat or diagnose
PT vespid venom sensitivity.
XX
PS Example 1; Fig 1; 73pp; English.
XX
CC This sequence represents vespid antigen 5s from yellowjacket. The
CC invention relates to peptides derived from vespid venom antigen 5 (VW5)
CC that are antigenic for T cell proliferation in mice immunised with VW5.
CC The peptides can be used to treat or diagnose vespid venom sensitivity
CC e.g. to Dolichovesputa maculata (white face hornet), Vesputa vulgaris
CC (yellowjacket), V. maculifrons (yellowjacket), D. arenaria (yellow
CC hornet), Polistes annularis (wasp), P. exclamans (wasp), V. crabro
CC (European hornet), V. flavopilosa (yellowjacket), V. germanica
CC (yellowjacket), V. pennsylvanica (yellowjacket), V. squamosa
CC (yellowjacket), V. vidua (yellowjacket) and P. fuscatus (paperwasp)
XX
SQ Sequence 204 AA;
Query Match 100.0%; Score 420; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2e-44;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVVSYGLTKQEKQDILKEHNDFRQKIARGLE 60
DB 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVVSYGLTKQEKQDILKEHNDFRQKIARGLE 60

QY 61 TRGNPGPPPAKNNKN 76
DB 61 TRGNPGPPPAKNNKN 76

RESULT 3
AAW45217
ID AAW45217 standard; protein; 204 AA.
XX
AC AAW45217;
XX
DT 05-JAN-2000 (first entry)
XX
DE Wild type wasp Ves v 5 protein sequence.
XX
KW Bet v 1; Ves v 5; pollen allergen; Fagales; Oleales; Pinales; mutant;
KW Hymenoptera; IgE; immunoglobulin E; vaccine; allergic reaction.
XX
OS Vesputa lewisii.
XX
PN WO9947680-A1.
XX
PD 23-SEP-1999.
XX
PF 16-MAR-1999; 99WO-DK000136.
XX
PR 16-MAR-1998; 98DK-00000364.
XX
PA (ALKA-) ALK-ABELLO AS.
XX
PI Ipsen HH, Spangfort MD, Larsen JN;
XX
DR WPI; 1999-601103/51.
XX
DR N-PSDB; AAZ25685.
XX
PT New mutated allergen with lower specific affinity to IgE, useful for
PT treatment of allergic reactions.
XX
PS Example 1; Fig 13; 77pp; English.
XX
CC The present invention describes a recombinant mutated allergen, with a
CC surface exposed substituted amino acid on a B-cell epitope. The
CC recombinant, non-natural, mutated allergen has at least one surface-
CC exposed conserved amino acid of a B-cell epitope substituted by another
CC amino acid, and essentially the same alpha-carbon backbone tertiary
CC structure as the naturally occurring allergen. The substituted amino acid
CC does not occur in the same position of any known homologous protein
CC within the taxonomic order of the natural allergen. Specific IgE binding
CC to the mutant is reduced compared to the naturally occurring allergen.
CC The recombinant allergen is used as a vaccine to treat, prevent or
CC alleviate allergic reactions. The present sequence represents the wild
CC type Ves v 5, which can have the following mutations: Lys72Ala and
CC Tyr96Ala
XX
SQ Sequence 204 AA;
Query Match 100.0%; Score 420; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2e-44;
Matches 76; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVVSYGLTKQEKQDILKEHNDFRQKIARGLE 60
DB 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVVSYGLTKQEKQDILKEHNDFRQKIARGLE 60

QY 61 TRGNPGPPPAKNNKN 76
DB 61 TRGNPGPPPAKNNKN 76

RESULT 4
ABG66983
ID ABG66983 standard; protein; 204 AA.
XX
AC ABG66983;
XX

```

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:52:17 ; Search time 105.878 Seconds
(without alignments)
315.390 Million cell updates/sec

Title: US-10-091-135-95
Perfect score: 420
Sequence: 1 NNYCKIKLKGVTACKYG.....RGLETRGNPGPPAKNMKN 76

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: geneseqp1980s.*
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3: geneseqp2000s.*
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5: geneseqp2002s.*
6: geneseqp2003as.*
7: geneseqp2003bs.*
8: geneseqp2004s.*
9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	420	100.0	76	AEE28829	Aee28829 Vesputa v
2	420	100.0	204	Aaw35688	Aaw35688 Vespid an
3	420	100.0	204	Aay45217	Aay45217 Wild type
4	420	100.0	204	ABG66983	ABG66983 Wasp veno
5	420	100.0	204	ABG67052	ABG67052 Wasp veno
6	420	100.0	204	ABG67104	ABG67104 Wasp veno
7	420	100.0	204	Aee28820	Aee28820 Vesputa v
8	420	100.0	209	ABM00031	ABM00031 Allergen
9	420	100.0	227	AAY25644	Aay25644 Vesputa s
10	420	100.0	227	ADC34893	ADC34893 Wasp alie
11	414	98.6	204	Aaw35687	Aaw35687 Vespid an
12	414	98.6	204	ABG66977	ABG66977 Wasp veno
13	414	98.6	204	ABG67103	ABG67103 Wasp veno
14	411	97.9	227	AAE13071	AAE13071 Vesputa v
15	347.5	82.7	206	AAY25648	Aay25648 Vesputa s
16	347.5	82.7	206	ADC34897	ADC34897 Wasp alie
17	313	74.5	57	Aee28828	Aee28828 Vesputa v
18	305	72.6	204	Aaw35691	Aaw35691 Vespid an
19	296.5	70.6	203	Aaw35689	Aaw35689 Vespid an
20	289	68.8	205	Aaw35690	Aaw35690 Vespid an
21	279	66.4	50	AAE28827	AAE28827 Vesputa v
22	254	60.5	46	Aee28812	Aee28812 Vesputa v
23	243	57.9	205	Aaw35693	Aaw35693 Vespid an
24	243	57.9	205	Aaw35692	Aaw35692 Vespid an

25	243	57.9	205	5	AAE28821	Aae28821 Polistes
26	220	52.4	39	5	AAE28811	Aae28811 Vesputa v
27	184	43.8	32	5	AAE28810	Aae28810 Vesputa v
28	180	42.9	31	2	AAW35648	Aaw35648 T cell pe
29	174	41.4	31	2	AAW35647	Aaw35647 T cell pe
30	168	40.0	31	2	AAW35656	Aaw35656 T cell pe
31	168	40.0	31	2	AAW35655	Aaw35655 T cell pe
32	153	36.4	162	5	AAE21099	Aae21099 Human epe
33	147	35.0	172	4	ABU53238	ABU53238 Human tes
34	142	33.8	31	2	AAW35657	Aaw35657 T cell pe
35	140	33.3	24	5	AAE28809	Aae28809 Vesputa v
36	139	33.1	31	2	AAW35659	Aaw35659 T cell pe
37	136	32.4	31	2	AAW35658	Aaw35658 T cell pe
38	135	32.1	30	2	AAW35645	Aaw35645 Immunomod
39	126	30.0	32	2	AAW35650	Aaw35650 T cell pe
40	125	29.8	31	2	AAW35660	Aaw35660 T cell pe
41	125	29.8	31	2	AAW35661	Aaw35661 T cell pe
42	124	29.5	32	2	AAW35651	Aaw35651 T cell pe
43	119	28.3	32	2	AAW35644	Aaw35644 Immunomod
44	112.5	26.8	31	2	AAW35649	Aaw35649 T cell pe
45	107	25.5	18	5	AAE28808	Aae28808 Vesputa v

ALIGNMENTS

RESULT 1

AAE28829	AAE28829 standard; peptide; 76 AA.
XX	AAE28829;
AC	AAE28829;
XX	27-DEC-2002 (first entry)
DT	27-DEC-2002 (first entry)
XX	Vesputa vulgaris antigen 5 (Ves V5) allergen peptide #16.
DE	Allergen; hybrid protein; allergenicity; immune system related disease;
XX	immunogenicity; allergy; vaccine; antigen 5.
KW	Vesputa vulgaris.
KW	WO200270665-A2.
OS	12-SEP-2002.
XX	04-MAR-2002; 2002WO-US006765.
PN	02-MAR-2001; 2001US-0272818P.
PD	(UYRQ) UNIV ROCKEFELLER.
PF	(ALKA-) ALK-ABELLO AS.
PR	King TP, Spangfort MD;
XX	WPI; 2002-698751/75.
XX	N-PSDB; AAD46274.
XX	New allergen hybrid protein having reduced allergenicity but retaining immunogenicity, useful for treating allergy or immune system related diseases.
XX	Claim 17; Page 152; 222pp; English.
XX	The present invention relates to recombinant allergen hybrid proteins having reduced allergenicity but retaining immunogenicity. The hybrid proteins comprise a peptide epitope sequence of an allergen protein and a scaffold protein that is structurally homologous to the allergen protein. Sequences of the invention comprise a native conformation and the peptide epitope sequence is present in a surface accessible region of the hybrid protein corresponding to its position in the allergen protein. The hybrid proteins are useful for treating allergy or immune system related diseases. They are also used as vaccines. The present sequence is Vesputa vulgaris antigen 5 (Ves V5) allergen peptide

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:08:42 ; Search time 12.4046 Seconds
(without alignments)
171.264 Million cell updates/sec

Title: US-10-091-135-93

Perfect score: 279

Sequence: 1 NNYCKIKLGGVHTACKYK.....VVSGLTKQEKQDILKEHND 50

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Published Applications AA New:*
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 - 2: /SIDSS5/ptodata/2/pubpaa/US06_NEW_PUB_PEP.*
 - 3: /SIDSS5/ptodata/2/pubpaa/US07_NEW_PUB_PEP.*
 - 4: /SIDSS5/ptodata/2/pubpaa/PCT_NEW_PUB_PEP.*
 - 5: /SIDSS5/ptodata/2/pubpaa/US03_NEW_PUB_PEP.*
 - 6: /SIDSS5/ptodata/2/pubpaa/US10_NEW_PUB_PEP.*
 - 7: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB_PEP.*
 - 8: /SIDSS5/ptodata/2/pubpaa/US60_NEW_PUB_PEP.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	279	100.0	227	6	US-10-498-026-76
2	215.5	77.2	206	6	US-10-498-026-80
3	65.5	23.5	2871	7	US-11-169-041-131
4	65.5	23.5	3002	6	US-10-821-234-916
5	64	22.9	271	6	US-10-533-811-1
6	61.5	22.0	298	7	US-11-124-367A-416
7	61.5	22.0	298	7	US-11-124-367A-417
8	61.5	22.0	298	7	US-11-124-367A-419
9	61.5	22.0	313	7	US-11-124-367A-418
10	61.5	22.0	416	7	US-11-124-367A-415
11	58	20.8	2911	7	US-11-090-617-706
12	56	20.1	365	7	US-11-108-528-56
13	56	20.1	365	7	US-11-108-528-58
14	54.5	19.5	236	6	US-10-527-500-65
15	54.5	19.5	277	6	US-10-527-500-23
16	54.5	19.5	543	7	US-11-106-672A-10
17	54.5	19.5	543	7	US-11-057-732-6
18	54.5	19.5	543	7	US-11-154-805A-5
19	54.5	19.5	592	7	US-11-106-672A-14
20	54	19.4	135	7	US-11-188-298-3692
21	54	19.4	245	7	US-11-188-298-8231
22	54	19.4	336	7	US-11-188-298-7686
23	54	19.4	1294	7	US-11-079-463-7534
24	53	19.0	253	7	US-11-172-740-561
25	52.5	18.8	996	7	US-11-079-463-6193

26	52	18.6	254	7	US-11-172-740-2285	Sequence 2285, Ap
27	52	18.6	254	7	US-11-188-298-19953	Sequence 19953, A
28	52	18.6	618	7	US-11-033-116-2	Sequence 2, Appli
29	52	18.6	1978	7	US-11-212-443-60	Sequence 60, Appli
30	51.5	18.5	199	6	US-10-793-626-1342	Sequence 1342, Ap
31	51.5	18.5	251	6	US-10-793-626-3050	Sequence 3050, Ap
32	51.5	18.5	299	7	US-11-188-298-17281	Sequence 17281, A
33	51	18.3	357	7	US-11-108-528-60	Sequence 60, Appli
34	51	18.3	359	7	US-11-108-528-62	Sequence 62, Appli
35	51	18.3	604	7	US-11-079-463-5436	Sequence 5436, Ap
36	51	18.3	643	7	US-11-096-568A-18660	Sequence 18660, A
37	51	18.3	851	7	US-11-096-568A-18659	Sequence 18659, A
38	51	18.3	872	7	US-11-096-568A-18658	Sequence 18658, A
39	50.5	18.1	320	7	US-11-079-463-8514	Sequence 8514, A
40	50	17.9	245	7	US-11-188-298-13741	Sequence 13741, A
41	50	17.9	342	6	US-10-491-468-8	Sequence 8, Appli
42	50	17.9	342	6	US-10-491-468-40	Sequence 40, Appli
43	50	17.9	381	6	US-10-689-742-172	Sequence 172, App
44	50	17.9	408	6	US-10-491-468-13	Sequence 13, Appli
45	50	17.9	408	7	US-11-072-512-2081	Sequence 2081, Ap

ALIGNMENTS

RESULT 1

US-10-498-026-76
; Sequence 76, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-76

Query Match 100.0%; Score 279; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 3.8e-29;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLGGVHTACKYGLKPCNCGNKVVSYGLTKQEKQDILKEHND 50
Db 24 NNYCKIKLGGVHTACKYGLKPCNCGNKVVSYGLTKQEKQDILKEHND 73

RESULT 2

US-10-498-026-80
; Sequence 80, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-80

Query Match 77.2%; Score 215.5; DB 6; Length 206;
Best Local Similarity 80.0%; Pred. No. 7.6e-21;
Matches 40; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

ORGANISM: Vesputula vulgaris
US-10-091-135-94

Query Match 100.0%; Score 279; DB 4; Length 57;
Best Local Similarity 100.0%; Pred. No. 4.8e-28;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQEKQDILKEHND 50
DB 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQEKQDILKEHND 50

RESULT 3
US-10-091-135-95
Sequence 95, Application US/10091135
Publication No. US20030039660A1
GENERAL INFORMATION:
APPLICANT: King, Te Piao
APPLICANT: Spangfort, Michael Dho
TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN
FILE REFERENCE: 2313/1H587-US1
CURRENT APPLICATION NUMBER: US/10/091,135
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: US 60/272,818
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn version 3.1
SEQ ID NO 95
LENGTH: 76
TYPE: PRT
ORGANISM: Vesputula vulgaris
US-10-091-135-95

Query Match 100.0%; Score 279; DB 4; Length 76;
Best Local Similarity 100.0%; Pred. No. 6.7e-28;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQEKQDILKEHND 50
DB 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQEKQDILKEHND 50

RESULT 4
US-10-001-245-119
Sequence 119, Application US/10001245
Publication No. US20030175312A1
GENERAL INFORMATION:
APPLICANT: HOLM, Jens
APPLICANT: IPSEN, Henrik
APPLICANT: LARSEN, Jorgen N.
APPLICANT: SPANGFORT, Michael D.
TITLE OF INVENTION: NO. US20030175312A1 mutant allergens
FILE REFERENCE: 4305/1H942-US2
CURRENT APPLICATION NUMBER: US/10/001,245
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/298,170
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/249,361
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn version 3.1
SEQ ID NO 119
LENGTH: 201
TYPE: PRT
ORGANISM: Vesputula
NAME/KEY: MISC FEATURE
LOCATION: (1)-(201)
OTHER INFORMATION: where X is any amino acid
US-10-001-245-119

Query Match 100.0%; Score 279; DB 4; Length 201;

Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQEKQDILKEHND 50
DB 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQEKQDILKEHND 50

RESULT 5
US-10-001-245-117
Sequence 117, Application US/10001245
Publication No. US20030175312A1
GENERAL INFORMATION:
APPLICANT: HOLM, Jens
APPLICANT: IPSEN, Henrik
APPLICANT: LARSEN, Jorgen N.
APPLICANT: SPANGFORT, Michael D.
TITLE OF INVENTION: NO. US20030175312A1 mutant allergens
FILE REFERENCE: 4305/1H942-US2
CURRENT APPLICATION NUMBER: US/10/001,245
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/298,170
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/249,361
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn version 3.1
SEQ ID NO 117
LENGTH: 202
TYPE: PRT
ORGANISM: Vesputula
NAME/KEY: MISC FEATURE
LOCATION: (1)-(202)
OTHER INFORMATION: where X is any amino acid
US-10-001-245-117

Query Match 100.0%; Score 279; DB 4; Length 202;
Best Local Similarity 100.0%; Pred. No. 2e-27;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQEKQDILKEHND 50
DB 1 NNYCKIKLKGCVHTACKYGLKPCNCGKVVVSYGLTKQEKQDILKEHND 50

RESULT 6
US-10-001-245-118
Sequence 118, Application US/10001245
Publication No. US20030175312A1
GENERAL INFORMATION:
APPLICANT: HOLM, Jens
APPLICANT: IPSEN, Henrik
APPLICANT: LARSEN, Jorgen N.
APPLICANT: SPANGFORT, Michael D.
TITLE OF INVENTION: NO. US20030175312A1 mutant allergens
FILE REFERENCE: 4305/1H942-US2
CURRENT APPLICATION NUMBER: US/10/001,245
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/298,170
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/249,361
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn version 3.1
SEQ ID NO 118
LENGTH: 203
TYPE: PRT
ORGANISM: Vesputula
NAME/KEY: MISC FEATURE
LOCATION: (1)-(203)
OTHER INFORMATION: where X is any amino acid
US-10-001-245-118

QY 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVVSYGLTKQEKQDILKEHND 50
DB 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVVSYGLTKQEKQDILKEHND 50

RESULT 2
US-08-614-935-2
Sequence 2, Application US/08614935
Patent No. 5804201
GENERAL INFORMATION:
APPLICANT: King, Te P.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Vespula vulgaris
US-09-130-287-2

Query Match 100.0%; Score 279; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.3e-27;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVVSYGLTKQEKQDILKEHND 50
DB 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVVSYGLTKQEKQDILKEHND 50

RESULT 4
US-09-541-759-6
Sequence 6, Application US/09541759
Patent No. 6723322
GENERAL INFORMATION:
APPLICANT: Lustigman, Sara
APPLICANT: Pearlman, Eric
APPLICANT: Umasch, Thomas
TITLE OF INVENTION: ANGIOGENIC ONCHOCERCA VOLVULUS PROTEINS AND USES THEREOF
FILE REFERENCE: 63475/252
CURRENT APPLICATION NUMBER: US/09/541,759
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patent in version 3.0
SEQ ID NO 6
LENGTH: 227
TYPE: PRT
ORGANISM: Vespula vulgaris
US-09-541-759-6

Query Match 100.0%; Score 279; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.4e-27;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVVSYGLTKQEKQDILKEHND 50

RESULT 2
US-08-614-935-2
Sequence 2, Application US/08614935
Patent No. 5804201
GENERAL INFORMATION:
APPLICANT: King, Te P.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Vespula vulgaris
US-08-614-935-2

Query Match 100.0%; Score 279; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.3e-27;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVVSYGLTKQEKQDILKEHND 50
DB 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVVSYGLTKQEKQDILKEHND 50

RESULT 3
US-09-130-287-2
Sequence 2, Application US/09130287
Patent No. 6106844
GENERAL INFORMATION:
APPLICANT: King, Te P.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:57:41 ; Search time 15.0763 Seconds
(without alignments)
274.190 Million cell updates/sec

Title: US-10-091-135-93
Perfect score: 279
Sequence: 1 NNYCKIKLKGVTACKYG.....VVSYGLTKQEKQDILKEHND 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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3: /cgn2_6/ptodata/1/iaa/H COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	ID	Description
1	279	100.0	204	1	US-08-419-414-9	Sequence 9, Appl
2	279	100.0	204	1	US-08-614-935-2	Sequence 2, Appl
3	279	100.0	204	1	US-09-130-287-2	Sequence 2, Appl
4	279	100.0	227	2	US-09-541-759-6	Sequence 6, Appl
5	273	97.8	204	1	US-08-614-935-1	Sequence 1, Appl
6	273	97.8	204	2	US-09-130-287-1	Sequence 1, Appl
7	190	68.1	204	1	US-08-614-935-5	Sequence 5, Appl
8	190	68.1	204	2	US-09-130-287-5	Sequence 5, Appl
9	180	64.5	31	1	US-08-614-935-46	Sequence 46, Appl
10	180	64.5	31	2	US-09-130-287-46	Sequence 46, Appl
11	174	62.4	31	1	US-08-614-935-45	Sequence 45, Appl
12	174	62.4	31	2	US-09-130-287-45	Sequence 45, Appl
13	171.5	61.5	203	1	US-08-419-414-8	Sequence 8, Appl
14	171.5	61.5	203	1	US-08-614-935-3	Sequence 3, Appl
15	171.5	61.5	203	1	US-08-130-287-3	Sequence 3, Appl
16	163	58.4	205	1	US-08-614-935-4	Sequence 4, Appl
17	163	58.4	205	2	US-09-130-287-4	Sequence 4, Appl
18	137	49.1	205	1	US-08-419-414-10	Sequence 10, Appl
19	137	49.1	205	1	US-08-614-935-6	Sequence 6, Appl
20	137	49.1	205	1	US-08-614-935-7	Sequence 7, Appl
21	137	49.1	205	2	US-09-130-287-6	Sequence 6, Appl
22	137	49.1	205	2	US-09-130-287-7	Sequence 7, Appl
23	126	45.2	32	1	US-08-614-935-48	Sequence 48, Appl
24	126	45.2	32	2	US-09-130-287-48	Sequence 48, Appl
25	124	44.4	32	1	US-08-614-935-49	Sequence 49, Appl
26	124	44.4	32	2	US-09-130-287-49	Sequence 49, Appl
27	119	42.7	32	1	US-08-614-935-42	Sequence 42, Appl

28	119	42.7	32	2	US-09-130-287-42	Sequence 42, Appl
29	112.5	40.3	31	1	US-08-614-935-47	Sequence 47, Appl
30	112.5	40.3	31	2	US-09-130-287-47	Sequence 47, Appl
31	94	33.7	34	1	US-08-614-935-50	Sequence 50, Appl
32	94	33.7	34	1	US-08-614-935-51	Sequence 51, Appl
33	94	33.7	34	2	US-09-130-287-50	Sequence 50, Appl
34	94	33.7	34	2	US-09-130-287-51	Sequence 51, Appl
35	88.5	31.7	20	1	US-08-614-935-8	Sequence 8, Appl
36	88.5	31.7	20	2	US-09-130-287-8	Sequence 8, Appl
37	76.5	27.4	20	1	US-08-614-935-9	Sequence 9, Appl
38	76.5	27.4	20	2	US-09-130-287-9	Sequence 9, Appl
39	73	26.2	20	1	US-08-614-935-10	Sequence 10, Appl
40	73	26.2	20	2	US-09-130-287-10	Sequence 10, Appl
41	72.5	26.0	34	1	US-08-614-935-33	Sequence 33, Appl
42	72.5	26.0	34	2	US-09-130-287-33	Sequence 33, Appl
43	70	25.1	20	1	US-08-614-935-11	Sequence 11, Appl
44	70	25.1	20	2	US-09-130-287-11	Sequence 11, Appl
45	65.5	23.5	1935	2	US-09-949-016-10403	Sequence 10403, A

ALIGNMENTS

RESULT 1
US-08-419-414-9
; Sequence 9, Application US/08419414
; Patent No. 5753787
; GENERAL INFORMATION:
; APPLICANT: Hawdon, John M.
; APPLICANT: Hotez, Peter J.
; APPLICANT: Jones, Brian F.
; TITLE OF INVENTION: Hookworm Vaccine
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,414
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Vespula vulgaris
US-08-419-414-9

Query Match 100.0%; Score 279; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.3e-27;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 1.2e-25; Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVSYGLTKQEKQDILKEHND 50
DB 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVSYGLTKQEKQDILKEHND 50

RESULT 2

VA5_VESVU STANDARD; PRT; 227 AA.
AC Q05110; Q9UB91;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Venom allergen 5 precursor (Antigen 5) (Ag5) (Allergen Ves v 5) (Ves v V).
OS Vespula vulgaris (Yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=7454;
RN (1)_TaxID=7454;
RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=93203603; PubMed=8454859;
RA Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
RT "Sequence analysis and antigenic cross-reactivity of a venom allergen, antigen 5, from hornets, wasps, and yellow jackets.";
RL J. Immunol. 150:2823-2830 (1993).
RN (2)
RP NUCLEOTIDE SEQUENCE OF 24-227.
RA Suck R., Hagen S., Fiebig H.;
RT "Molecular cloning of a genomic sequence from the venom allergen antigen 5 from Vespula vulgaris.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the CRISP family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
DR EMBL; M98958; AAA30333.1; -; mRNA.
DR EMBL; AJ238849; CAB42887.1; -; Genomic DNA.
DR PDB; 1QNX; X-ray; A=24-227.
DR InterPro; IPR001283; Allrgn_V5/Tpx1.
DR InterPro; IPR002413; V5_allergen.
DR Pfam; PF00188; SCP; 1.
DR PRINTS; PR00838; V5ALLERGEN.
DR PRINTS; PR00837; V5TPXLKE.
DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
DR SMART; SM00198; SCP; 1.
DR PROSITE; PS01009; CRISP_1; 1.
DR PROSITE; PS01010; CRISP_2; 1.
KW 3D-structure; Allergen; Direct protein sequencing; Signal.
FT SIGNAL 1 23
FT CHAIN 24 227 Venom allergen 5.
FT DISULFD 27 40 By similarity.
FT DISULFD 31 124 By similarity.
FT DISULFD 49 117 By similarity.
FT DISULFD 193 210 By similarity.
FT CONFLICT 109 109 V -> I (in Ref. 2).
FT CONFLICT 118 118 Q -> E (in Ref. 2).
FT CONFLICT 173 173 D -> N (in Ref. 2).
FT CONFLICT 219 219 M -> K (in Ref. 2).
FT HELIX 26 28
FT TURN 32 33
FT HELIX 38 41
FT STRAND 53 57

FT HELIX 61 79
FT TURN 80 81
FT TURN 87 88
FT STRAND 94 94
FT STRAND 101 102
FT HELIX 104 114
FT TURN 115 116
FT STRAND 133 141
FT HELIX 149 157
FT HELIX 158 162
FT TURN 165 166
FT HELIX 169 171
FT HELIX 174 183
FT TURN 184 184
FT TURN 186 187
FT STRAND 190 200
FT TURN 201 202
FT STRAND 203 213
FT TURN 219 220
FT STRAND 226 227
SQ SEQUENCE 227 AA; 25798 MW; 99E9813740A66F55 CRC64;

Query Match . 100.0%; Score 279; DB 1; Length 227;

Best Local Similarity 100.0%; Pred. No. 1.3e-25; Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCNGKVVSYGLTKQEKQDILKEHND 50
DB 24 NNYCKIKLKGCVHTACKYGLKPCNGKVVSYGLTKQEKQDILKEHND 73

RESULT 3

VA5_VESPE STANDARD; PRT; 204 AA.
AC P35785;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves p 5) (Ves p V).
OS Vespula pensylvanica (Western yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=30213;
RN (1)
RP PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94044316; PubMed=8227862;
RA Hoffman D.R.;
RT "Allergens in Hymenoptera venom. XXV: the amino acid sequences of antigen 5 molecules and the structural basis of antigenic cross-reactivity.";
RL J. Allergy Clin. Immunol. 92:707-716 (1993).
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the CRISP family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC PIR; C44583; C44583.
CC HSSP; Q05110; 1QNX.
CC SMR; F35785; 1-204.
CC InterPro; IPR001283; Allrgn_V5/Tpx1.
CC InterPro; IPR002413; V5_allergen.
CC Pfam; PF00188; SCP; 1.
CC PRINTS; PR00838; V5ALLERGEN.
CC PRINTS; PR00837; V5TPXLKE.
CC ProDom; PD000542; Allrgn_V5/Tpx1; 1.
CC SMART; SM00198; SCP; 1.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:53:37 ; Search time 73.855 Seconds
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477.644 Million cell updates/sec

Title: US-10-091-135-93
Perfect score: 279
Sequence: 1 NNYCKIRKLGKGVHTACKYG.....VVSYGLTKQEKQDILKEHND 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	279	100.0	204	1	VAS_VESFL
2	279	100.0	227	1	VAS_VESVU
3	275	98.6	204	1	VAS_VESPE
4	273	97.8	204	1	VAS_VESMC
5	256	91.8	204	1	VAS_VESGE
6	215.5	77.2	205	1	VAS_VESQV
7	215.5	77.2	206	1	VAS_VESVI
8	190	68.1	227	1	VAS2_DOLMA
9	182	65.2	202	1	VAS1_VESCR
10	182	65.2	202	1	VAS2_VESCR
11	177	63.4	202	1	VAS_VESMA
12	171.5	61.5	203	1	VAS_DOLAR
13	161	57.7	215	1	VAS3_DOLMA
14	146	52.3	206	1	VAS_POLGA
15	143	51.3	206	1	VAS_POLDQ
16	143	51.3	227	2	Q68KJ9_POLDQ
17	139	49.8	205	1	VAS_POLFU
18	137	49.1	205	1	VAS_POLEX
19	137	49.1	209	1	VAS_POLAN
20	134	48.0	226	2	Q68KJ9_POLEX
21	120.5	43.2	207	1	VAS_POISR
22	77	27.6	211	1	VAS_SOLRI
23	77	27.6	234	1	VAS3_SOLIN
24	70.5	25.3	2500	2	Q96223_PLAF7
25	69.5	24.9	401	2	Q97LG9_CLOAB
26	69.5	24.9	525	2	Q9DWE1_RCMVM
27	67.5	24.2	283	2	Q7Q991_ANOGA
28	67.5	24.2	610	2	Q54FR6_DICDI
29	67.5	24.2	2884	2	Q4SHN1_TETNG
30	67	24.0	2025	2	Q9SHK4_ARATH
31	66	23.7	3429	2	Q81BP1_PLAF7

32	65.5	23.5	195	2	Q75N89_HUMAN	Q75N89 homo sapien
33	65.5	23.5	307	2	Q7RA91_PLAYO	Q7RA91 plasmodium
34	65.5	23.5	1095	2	Q60784_MOUSE	Q60784 mus musculus
35	65.5	23.5	1295	1	GLP1_CAEEL	P13508 caenorhabdi
36	65.5	23.5	1365	2	Q75N88_HUMAN	Q75N88 homo sapien
37	65.5	23.5	2871	1	FBN1_BOVIN	P98133 bos taurus
38	65.5	23.5	2871	1	FBN1_MOUSE	P35555 homo sapien
39	65.5	23.5	2871	1	FBN1_PIG	Q61554 sus scrofa
40	65.5	23.5	2871	1	Q75N87_HUMAN	Q75N87 homo sapien
41	65.5	23.5	2872	2	Q9WU88_RAT	Q9WU88 rattus norv
42	65.5	23.5	3857	2	O88840_MOUSE	O88840 mus musculus
43	64.5	23.1	415	2	Q54YC8_DICDI	Q54YC8 dictyosteli
44	64	22.9	271	2	Q9XZ44_LUTLO	Q9XZ44 lutzomyia l

ALIGNMENTS

RESULT 1
ID - VAS_VESFL STANDARD; PRT; 204 AA.
AC P35783;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves f 5) (Ves f V).
OS Vespula flavopilosa (Yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
OX NCBI_TaxID=30211;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94044316; PubMed=8227862;
RA Hofman D.R.;
RT "Allergens in Hymenoptera venom. XXV: the amino acid sequences of
RT antigen 5 molecules and the structural basis of antigenic cross-
RT reactivity.";
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -!- FUNCTION: May have an ancestral function in the promotion of ovum
CC fertilization by sperm.
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the CRISP family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC PIR; A44583; A44583.
CC HSP; Q05110; IQNX.
CC SMR; P35783; 1-204.
CC InterPro; IPR001283; Allrgn_V5/Tpx1.
CC InterPro; IPR002413; V5_allergen.
CC Pfam; PF00188; SCP; 1.
CC PRINTS; PR00838; V5ALLERGEN.
CC PRINTS; PD00837; V5TPXLIKE.
CC ProDom; PD000542; Allrgn_V5/Tpx1; 1.
CC SMART; SM00198; SCP; 1.
CC PROSITE; PS01009; CRISP_1; 1.
CC PROSITE; PS01010; CRISP_2; 1.
CC Allergen; Direct protein sequencing.
KW Allergen; By similarity.
FT DISULFID 4 17 By similarity.
FT DISULFID 8 101 By similarity.
FT DISULFID 26 94 By similarity.
FT DISULFID 170 187 By similarity.
SQ SEQUENCE 204 AA; 23274 MW; 7667232536AB2FC5 CRC64;
Query Match 100.0%; Score 279; DB 1; Length 204;

RESULT 3

B37329
antigen 5 - eastern yellowjacket
C:Species: Vespula maculifrons (eastern yellowjacket)
C:Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C:Accession: B37329
R:Lu, G.; Villalba, M.; Coccia, M.R.; Hoffman, D.R.; King, T.P.
submitted to the Protein Sequence Database, August 1992
A:Reference number: A37329
A:Accession: B37329
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <LUI>
A:Cross-references: UNIPROT:P35760; UNIPARC:UPI0000138092
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 97.8%; Score 273; DB 2; Length 204;
Best Local Similarity 98.0%; Pred. No. 7e-25;
Matches 49; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Dy 1 NNYCKIKLKGCVHTACKYGLSKPNCNGKVVVSYGLTKQEKQDILKEHND 50
1 NNYCKIKLKGCVHTACKYGLSKPNCNGKVVVSYGLTKQEKQDILKEHND 50

RESULT 4

B44583
venom allergen antigen Ves g 5 - German yellowjacket
C:Species: Vespula germanica (German yellowjacket)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: B44583; A44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV; the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: B44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
A:Cross-references: UNIPROT:P35784; UNIPARC:UPI0000138090
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 91.8%; Score 256; DB 2; Length 204;
Best Local Similarity 92.0%; Pred. No. 7.1e-23;
Matches 46; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Dy 1 NNYCKIKLKGCVHTACKYGLSKPNCNGKVVVSYGLTKQEKQDILKEHND 50
1 NNYCKIKLKGCVHTACKYGLSKPNCNGKVVVSYGLTKQEKQDILKEHND 50

RESULT 5

D44583
venom allergen antigen Ves s 5 - southern yellowjacket
C:Species: Vespula squamosa (southern yellowjacket)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: D44583; D44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV; the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: D44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-205 <HOF>
A:Cross-references: UNIPROT:P35786; UNIPARC:UPI0000138094
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 77.2%; Score 215.5; DB 2; Length 205;
Best Local Similarity 80.0%; Pred. No. 4.4e-18;
Matches 40; Conservative 4; Mismatches 5; Indels 1; Gaps 1;
Dy 2 NYCKIKLKGCVHTACKYGLSKPNCNGKVVVSYGLTKQEKQDILKEHND 50

Db 2 DYCKIKLKGCVHTACKYGLSKPNCNGKVVVSYGLTKQEKQDILKEHND 51

RESULT 6

E44583
venom allergen antigen Ves vi 5 - yellowjacket (Vespula vidua)
C:Species: Vespula vidua
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: E44583; E44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993

A:Title: Allergens in hymenoptera venom XXV; the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: E44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-206 <HOF>
A:Cross-references: UNIPROT:P35787; UNIPARC:UPI0000138095
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 77.2%; Score 215.5; DB 2; Length 206;
Best Local Similarity 80.0%; Pred. No. 4.4e-18;
Matches 40; Conservative 3; Mismatches 6; Indels 1; Gaps 1;
Dy 2 NYCKIKLKGCVHTACKYGLSKPNCNGKVVVSYGLTKQEKQDILKEHND 50
3 NYCKIKLKGCVHTACKYGLSKPNCNGKVVVSYGLTKQEKQDILKEHND 52

RESULT 7

A31085
antigen 5-2 precursor - bald-faced hornet
C:Species: Vespula maculata (bald-faced hornet)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
C:Accession: A31085
R:Pang, K.S.Y.; Vitale, M.; Fehner, P.; King, T.P.
Proc. Natl. Acad. Sci. U.S.A. 85, 895-899, 1988
A:Title: cDNA cloning and primary structure of a white-face hornet venom allergen, ant
A:Reference number: A94213; MUID:88124947; PMID:3422469
A:Accession: A31085
A:Molecule type: mRNA
A:Residues: 1-227 <FAN>
A:Cross-references: UNIPROT:P10736; UNIPARC:UPI000013807D; GB:J03601; NID:G156714; PID:
C:Superfamily: yellowjacket venom allergen antigen 5
F:1-23/Domain: signal sequence #status predicted <SIG>
F:24-227/Product: antigen 5-2 #status predicted <MAT>

Query Match 68.1%; Score 190; DB 2; Length 227;
Best Local Similarity 68.6%; Pred. No. 5e-15;
Matches 35; Conservative 5; Mismatches 9; Indels 2; Gaps 2;
Dy 1 NNYCKIKLKGCVHTACKYGLSKPNCNGKVVVSYGLTKQEKQDILKEHND 50
24 NYCKIKLKGCVHTACKYGLSKPNCNGKVVVSYGLTKQEKQDILKEHND 73

RESULT 8

H44583
venom allergen antigen Vesp c 5.02 - European hornet
C:Species: Vespula crabro (European hornet)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: H44583; H44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV; the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: H44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-202 <HOF>
A:Cross-references: UNIPROT:P35782; UNIPARC:UPI0000138080
C:Superfamily: yellowjacket venom allergen antigen 5

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:56:21 ; Search time 10.4962 Seconds
(without alignments)
458.342 Million cell updates/sec

Title: US-10-091-135-93
Perfect score: 279
Sequence: 1 NNYCKIKLGGVHTACKYG.....VWSYGLTKQEKQDILKEHND 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80.*
1: PIR1.*
2: PIR2.*
3: PIR3.*
4: PIR4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	279	100.0	204	2 A44583	venom allergen ant
2	275	98.6	204	2 C44583	venom allergen ant
3	273	97.8	204	2 B37329	antigen 5 - easter
4	256	91.8	204	2 B44583	venom allergen ant
5	215.5	77.2	205	2 D44583	venom allergen ant
6	215.5	77.2	206	2 A44583	antigen 5-2 precu
7	190	68.1	227	2 A31085	venom allergen ant
8	182	65.2	202	2 H44583	venom allergen ant
9	182	65.2	202	2 G44583	antigen 5-3 precu
10	163	58.4	213	2 B31085	venom allergen ant
11	139	49.8	205	2 F44583	antigen 5 - paper
12	137	49.1	205	2 A37329	venom allergen Sol
13	77	27.6	211	2 B58853	venom allergen III
14	77	27.6	212	2 B37330	hypothetical prote
15	70.5	25.3	2500	2 G71609	hypothetical prote
16	69.5	24.9	401	2 G96972	protein f12k11.6 [
17	67	24.0	2025	2 D96201	glp1 protein precu
18	65.5	23.5	1295	2 A32901	fibrillin I - bovi
19	65.5	23.5	2871	2 A55567	fibrillin-1 precu
20	65.5	23.5	2871	2 A55624	fibrillin I precu
21	65.5	23.5	3002	2 A47221	hypothetical prote
22	63.5	22.8	292	2 H81857	hypothetical prote
23	63.5	22.8	342	2 B81086	hypothetical prote
24	60.5	21.7	1469	2 T19459	enterotoxin D prec
25	58.5	21.0	258	2 A33953	fibrillin-2 precu
26	58.5	21.0	2907	2 A57278	probable membrane
27	58.5	21.0	4910	2 S64942	masking protein pr
28	58	20.8	1712	2 A38261	fibrillin-2 precu
29	58	20.8	2918	2 A54105	

ALIGNMENTS

RESULT 1

A44583
venom allergen antigen Ves f 5 - yellowjacket (Vespula flavopilosa)
C:Species: Vespula Flavopilosa
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A44583; B44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: A44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
A:Cross-references: UNIPROT:P35783; UNIPARC:UPI000013808F
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 100.0%; Score 279; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 1.4e-25;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLGGVHTACKYGLKPKNCNKVVSYGLTKQEKQDILKEHND 50
|||||
Db 1 NNYCKIKLGGVHTACKYGLKPKNCNKVVSYGLTKQEKQDILKEHND 50

RESULT 2

C44583
venom allergen antigen Ves p 5 - western yellowjacket
C:Species: Vespula pensylvanica (western yellowjacket)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: C44583; C44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mole
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: C44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
A:Cross-references: UNIPROT:P35785; UNIPARC:UPI0000138093
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 98.6%; Score 275; DB 2; Length 204;
Best Local Similarity 96.0%; Pred. No. 4.1e-25;
Matches 48; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLGGVHTACKYGLKPKNCNKVVSYGLTKQEKQDILKEHND 50
|||||
Db 1 NNYCKIKLGGVHTACKYGLKPKNCNKVVSYGLTKQEKQDILKEHND 50

lipopolysaccharide
probable serine/th
secreted protein p
two-component sens
hypothetical prote
PINT domain protei
nucleoscapid prote
hypothetical prote
hypothetical prote
G2-G1 polypeptide
MADS box protein A
cysteine-rich prot
acid phosphatase (
hemagglutinin-neur
minor inner core p
probable sugar-nuc

```

XX SQ Sequence 50 AA;
Query Match 100.0%; Score 279; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 9.4e-28; Mismatches 0; Indels 0; Gaps 0;
Matches 50; Conservative 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVVSYGLTKQEKQDILKEHND 50
    |||||
DB 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVVSYGLTKQEKQDILKEHND 50

RESULT 2
AAE28828
ID AAE28828 standard; peptide; 57 AA.
XX
AC AAE28828;
XX
DT 27-DEC-2002 (first entry)
XX
DE Vesputa vulgaris antigen 5 (Ves V5) allergen peptide #15.
XX
Allergen; hybrid protein; allergenicity; immune system related disease;
KW immunogenicity; allergy; vaccine; antigen 5.
XX
OS Vesputa vulgaris.
XX
PN WO200270665-A2.
XX
PD 12-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006765.
XX
PR 02-MAR-2001; 2001US-0272818P.
XX
(UYRQ ) UNIV ROCKEFELLER.
PA (ALKA-) ALK-ABELLO AS.
XX
PI King TP, Spangfort MD;
XX
WPI; 2002-698751/75.
DR N-PSDB; AAD46273.
XX
New allergen hybrid protein having reduced allergenicity but retaining
PT immunogenicity, useful for treating allergy or immune system related
PT diseases.
XX
PS Claim 17; Page 152; 222pp; English.
XX
The present invention relates to recombinant allergen hybrid proteins
CC having reduced allergenicity but retaining immunogenicity. The hybrid
CC proteins comprise a peptide epitope sequence of an allergen protein and a
CC scaffold protein that is structurally homologous to the allergen protein.
CC Sequences of the invention comprise a native conformation and the peptide
CC epitope sequence is present in a surface accessible region of the hybrid
CC protein corresponding to its position in the allergen protein. The hybrid
CC proteins are useful for treating allergy or immune system related
CC diseases. They are also used as vaccines. The present sequence is Vesputa
CC vulgaris antigen 5 (Ves V5) allergen peptide
XX
SQ Sequence 57 AA;
Query Match 100.0%; Score 279; DB 5; Length 57;
Best Local Similarity 100.0%; Pred. No. 1.1e-27; Mismatches 0; Indels 0; Gaps 0;
Matches 50; Conservative 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVVSYGLTKQEKQDILKEHND 50
    |||||
DB 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVVSYGLTKQEKQDILKEHND 50

RESULT 3
AAE28829
ID AAE28829 standard; peptide; 76 AA.
XX
AC AAE28829;
XX
DT 27-DEC-2002 (first entry)
XX
DE Vesputa vulgaris antigen 5 (Ves V5) allergen peptide #16.
XX
Allergen; hybrid protein; allergenicity; immune system related disease;
KW immunogenicity; allergy; vaccine; antigen 5.
XX
OS Vesputa vulgaris.
XX
PN WO200270665-A2.
XX
PD 12-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006765.
XX
PR 02-MAR-2001; 2001US-0272818P.
XX
(UYRQ ) UNIV ROCKEFELLER.
PA (ALKA-) ALK-ABELLO AS.
XX
PI King TP, Spangfort MD;
XX
WPI; 2002-698751/75.
DR N-PSDB; AAD46274.
XX
New allergen hybrid protein having reduced allergenicity but retaining
PT immunogenicity, useful for treating allergy or immune system related
PT diseases.
XX
PS Claim 17; Page 152; 222pp; English.
XX
The present invention relates to recombinant allergen hybrid proteins
CC having reduced allergenicity but retaining immunogenicity. The hybrid
CC proteins comprise a peptide epitope sequence of an allergen protein and a
CC scaffold protein that is structurally homologous to the allergen protein.
CC Sequences of the invention comprise a native conformation and the peptide
CC epitope sequence is present in a surface accessible region of the hybrid
CC protein corresponding to its position in the allergen protein. The hybrid
CC proteins are useful for treating allergy or immune system related
CC diseases. They are also used as vaccines. The present sequence is Vesputa
CC vulgaris antigen 5 (Ves V5) allergen peptide
XX
SQ Sequence 76 AA;
Query Match 100.0%; Score 279; DB 5; Length 76;
Best Local Similarity 100.0%; Pred. No. 1.5e-27; Mismatches 0; Indels 0; Gaps 0;
Matches 50; Conservative 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVVSYGLTKQEKQDILKEHND 50
    |||||
DB 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVVSYGLTKQEKQDILKEHND 50

RESULT 4
AAW35688
ID AAW35688 standard; peptide; 204 AA.
XX
AC AAW35688;
XX
DT 13-MAY-1998 (first entry)
XX
DE Vespid antigen 5s from Vesputa vulgaris (yellowjacket).
XX
Immunomodulatory peptide; vespid antigen 5; immunogenic; allergy;
KW vespid venom; white face hornet wasp; immunodominant peptide; 1 cell.
XX
OS Vesputa vulgaris.
XX
PN WO9733910-A1.

```

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:52:17 ; Search time 69.6565 Seconds
(without alignments)
315.390 Million cell updates/sec

Title: US-10-091-135-93
Perfect score: 279
Sequence: 1 NNYCKIKLGGVHTACKYG.....VVSYLTKQEKQDILKEHND 50

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 21:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*
- 9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	279	100.0	50	AAE28827	Aae28827 Vespula v
2	279	100.0	57	AAE28828	Aae28828 Vespula v
3	279	100.0	76	AAE28829	Aae28829 Vespula v
4	279	100.0	204	AAW35688	Aaw35688 Vespul an
5	279	100.0	204	AAW45217	Aay45217 Wild type
6	279	100.0	204	ABG66983	Abg66983 Wasp veno
7	279	100.0	204	ABG67052	Abg67052 Wasp veno
8	279	100.0	204	ABG67104	Abg67104 Wasp veno
9	279	100.0	204	ABG67103	Abg67103 Wasp veno
10	279	100.0	204	AAE28820	Aae28820 Vespula v
11	279	100.0	209	ABM00031	Abm00031 Allergen
12	279	100.0	227	AAV25644	Aav25644 Vespula s
13	279	100.0	227	AAE13071	Aae13071 Vespula v
14	279	100.0	227	ADC34893	Adc34893 Wasp alle
15	273	97.8	204	AAW35687	Aaw35687 Vespul an
16	273	97.8	204	ABG66977	Abg66977 Wasp veno
17	254	91.0	46	AAE28812	Aae28812 Vespula v
18	220	78.9	39	AAE28811	Aae28811 Vespula v
19	215.5	77.2	206	AAV25648	Aav25648 Vespula s
20	215.5	77.2	206	ADC34897	Adc34897 Wasp alle
21	190	68.1	204	AAW35691	Aaw35691 Vespul an
22	184	65.9	32	AAE28810	Aae28810 Vespula v
23	180	64.5	31	AAW35648	Aaw35648 T cell pe
24	174	62.4	31	AAW35647	Aaw35647 T cell pe

ALIGNMENTS

RESULT 1					
AAE28827					
ID	AAE28827	standard;	peptide;	50 AA.	
XX	AAE28827;				
AC	AAE28827;				
XX					
DT	27-DEC-2002	(first entry)			
XX					
DE	Vespula vulgaris	antigen 5 (Ves V5)	allergen peptide #14.		
XX					
KW	Allergen;	hybrid protein;	allergen;	immunity;	immune system related disease;
KX	immunogenicity;	allergy;	vaccine;	antigen 5.	
XX					
OS	Vespula	vulgaris.			
XX					
FN	WO200270665-A2.				
XX					
PD	12-SEP-2002.				
XX					
PF	04-MAR-2002;	2002WO-US006765.			
XX					
PR	02-MAR-2001;	2001US-0272818P.			
XX					
PA	(UYRQ) UNIV ROCKEFELLER.				
PA	(ALKA-) ALK-ABELLO AS.				
XX					
PI	King TP, Spangfort MD;				
XX					
DR	WPI; 2002-698751/75.				
XX	N-PSDB; AAD46272.				
XX					
PT	New allergen hybrid protein	having reduced allergenicity	but retaining		
PT	immunogenicity;	useful for treating	allergy or immune system related		
XX	diseases.				
PS	Claim 17; Page 152;	222pp;	English.		
XX					
CC	The present invention relates to recombinant allergen hybrid proteins				
CC	having reduced allergenicity but retaining immunogenicity. The hybrid				
CC	proteins comprise a peptide epitope sequence of an allergen protein and a				
CC	scaffold protein that is structurally homologous to the allergen protein.				
CC	Sequences of the invention comprise a native conformation and the peptide				
CC	epitope sequence is present in a surface accessible region of the hybrid				
CC	protein corresponding to its position in the allergen protein. The hybrid				
CC	proteins are useful for treating allergy or immune system related				
CC	diseases. They are also used as vaccines. The present sequence is Vespula				
CC	vulgaris antigen 5 (Ves V5) allergen peptide				

99	29	54.7	297	6	US-10-878-556A-119	Sequence 119, App	172	29	54.7	306	7	US-11-002-387-50	Sequence 50, Appl
100	29	54.7	297	7	US-11-096-568A-3089	Sequence 3089, App	173	29	54.7	306	7	US-11-002-387-51	Sequence 51, Appl
101	29	54.7	297	7	US-11-188-298-2744	Sequence 2744, App	174	29	54.7	306	7	US-11-002-387-52	Sequence 52, Appl
102	29	54.7	297	7	US-11-188-298-4525	Sequence 4525, App	175	29	54.7	306	7	US-11-002-387-53	Sequence 53, Appl
103	29	54.7	305	7	US-11-187-687-9	Sequence 9, Appl	176	29	54.7	306	7	US-11-002-387-54	Sequence 54, Appl
104	29	54.7	305	7	US-11-187-687-10	Sequence 10, Appl	177	29	54.7	306	7	US-11-002-387-55	Sequence 55, Appl
105	29	54.7	305	7	US-11-187-687-11	Sequence 11, Appl	178	29	54.7	306	7	US-11-002-387-56	Sequence 56, Appl
106	29	54.7	306	6	US-10-530-421-18	Sequence 18, Appl	179	29	54.7	306	7	US-11-002-387-57	Sequence 57, Appl
107	29	54.7	306	6	US-10-530-421-19	Sequence 19, Appl	180	29	54.7	306	7	US-11-002-387-58	Sequence 58, Appl
108	29	54.7	306	6	US-10-530-421-20	Sequence 20, Appl	181	29	54.7	306	7	US-11-002-387-59	Sequence 59, Appl
109	29	54.7	306	7	US-11-017-550-35	Sequence 35, Appl	182	29	54.7	306	7	US-11-002-387-60	Sequence 60, Appl
110	29	54.7	306	7	US-11-017-550-37	Sequence 37, Appl	183	29	54.7	306	7	US-11-002-387-61	Sequence 61, Appl
111	29	54.7	306	7	US-11-017-550-38	Sequence 38, Appl	184	29	54.7	306	7	US-11-002-387-62	Sequence 62, Appl
112	29	54.7	306	7	US-11-017-550-39	Sequence 39, Appl	185	29	54.7	306	7	US-11-002-387-63	Sequence 63, Appl
113	29	54.7	306	7	US-11-017-550-40	Sequence 40, Appl	186	29	54.7	306	7	US-11-002-387-64	Sequence 64, Appl
114	29	54.7	306	7	US-11-017-550-41	Sequence 41, Appl	187	29	54.7	306	7	US-11-232-425-2	Sequence 2, Appl
115	29	54.7	306	7	US-11-017-550-42	Sequence 42, Appl	188	29	54.7	306	7	US-11-232-425-4	Sequence 4, Appl
116	29	54.7	306	7	US-11-017-550-43	Sequence 43, Appl	189	29	54.7	306	7	US-11-232-425-6	Sequence 6, Appl
117	29	54.7	306	7	US-11-017-550-44	Sequence 44, Appl	190	29	54.7	306	7	US-11-232-425-8	Sequence 8, Appl
118	29	54.7	306	7	US-11-017-550-45	Sequence 45, Appl	191	29	54.7	306	7	US-11-232-425-10	Sequence 10, Appl
119	29	54.7	306	7	US-11-017-550-46	Sequence 46, Appl	192	29	54.7	306	7	US-11-232-425-12	Sequence 12, Appl
120	29	54.7	306	7	US-11-017-550-47	Sequence 47, Appl	193	29	54.7	306	7	US-11-232-425-14	Sequence 14, Appl
121	29	54.7	306	7	US-11-017-550-48	Sequence 48, Appl	194	29	54.7	306	7	US-11-232-425-16	Sequence 16, Appl
122	29	54.7	306	7	US-11-017-550-49	Sequence 49, Appl	195	29	54.7	306	7	US-11-232-425-18	Sequence 18, Appl
123	29	54.7	306	7	US-11-017-550-50	Sequence 50, Appl	196	29	54.7	306	7	US-11-232-425-21	Sequence 21, Appl
124	29	54.7	306	7	US-11-017-550-51	Sequence 51, Appl	197	29	54.7	306	7	US-11-232-425-22	Sequence 22, Appl
125	29	54.7	306	7	US-11-017-550-52	Sequence 52, Appl	198	29	54.7	306	7	US-11-232-425-23	Sequence 23, Appl
126	29	54.7	306	7	US-11-017-550-53	Sequence 53, Appl	199	29	54.7	306	7	US-11-232-425-24	Sequence 24, Appl
127	29	54.7	306	7	US-11-017-550-54	Sequence 54, Appl	200	29	54.7	306	7	US-11-232-425-25	Sequence 25, Appl
128	29	54.7	306	7	US-11-017-550-55	Sequence 55, Appl	201	29	54.7	320	7	US-11-087-099-1916	Sequence 1916, App
129	29	54.7	306	7	US-11-017-550-56	Sequence 56, Appl	202	29	54.7	329	7	US-11-188-298-1902	Sequence 1902, App
130	29	54.7	306	7	US-11-017-550-57	Sequence 57, Appl	203	29	54.7	329	7	US-11-096-568A-3311	Sequence 3311, App
131	29	54.7	306	7	US-11-017-550-58	Sequence 58, Appl	204	29	54.7	354	6	US-10-838-616-2	Sequence 2, Appl
132	29	54.7	306	7	US-11-017-550-59	Sequence 59, Appl	205	29	54.7	354	7	US-11-096-568A-3310	Sequence 3310, App
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134	29	54.7	306	7	US-11-017-550-61	Sequence 61, Appl	207	29	54.7	380	7	US-11-096-568A-3091	Sequence 3091, App
135	29	54.7	306	7	US-11-017-550-62	Sequence 62, Appl	208	29	54.7	385	7	US-11-079-463-8871	Sequence 8871, App
136	29	54.7	306	7	US-11-017-550-63	Sequence 63, Appl	209	29	54.7	394	7	US-11-096-568A-3451	Sequence 3451, App
137	29	54.7	306	7	US-11-017-550-64	Sequence 64, Appl	210	29	54.7	434	7	US-11-188-298-13808	Sequence 13808, A
138	29	54.7	306	7	US-11-014-402-1	Sequence 1, Appl	211	29	54.7	456	6	US-10-467-657-4150	Sequence 4150, App
139	29	54.7	306	7	US-11-014-402-2	Sequence 2, Appl	212	29	54.7	463	7	US-11-072-512-2880	Sequence 2880, App
140	29	54.7	306	7	US-11-014-402-3	Sequence 3, Appl	213	29	54.7	474	6	US-10-793-626-946	Sequence 946, App
141	29	54.7	306	7	US-11-014-402-4	Sequence 4, Appl	214	29	54.7	499	7	US-11-188-298-12386	Sequence 12386, A
142	29	54.7	306	7	US-11-014-402-5	Sequence 5, Appl	215	29	54.7	500	7	US-11-072-512-3456	Sequence 3456, App
143	29	54.7	306	7	US-11-014-402-6	Sequence 6, Appl	216	29	54.7	559	7	US-11-072-512-2597	Sequence 2597, App
144	29	54.7	306	7	US-11-137-850-3	Sequence 3, Appl	217	29	54.7	664	6	US-10-793-626-346	Sequence 346, App
145	29	54.7	306	7	US-11-137-850-4	Sequence 4, Appl	218	29	54.7	690	7	US-11-052-554A-232	Sequence 232, App
146	29	54.7	306	7	US-11-137-850-6	Sequence 6, Appl	219	29	54.7	1083	7	US-11-079-463-9521	Sequence 9521, App
147	29	54.7	306	7	US-11-187-687-7	Sequence 7, Appl	220	29	54.7	1186	7	US-11-096-568A-33275	Sequence 33275, A
148	29	54.7	306	7	US-11-187-687-8	Sequence 8, Appl	221	29	54.7	1202	7	US-11-096-568A-33273	Sequence 33273, A
149	29	54.7	306	7	US-11-187-687-12	Sequence 12, Appl	222	29	54.7	1218	6	US-10-450-224A-2	Sequence 2, Appl
150	29	54.7	306	7	US-11-187-687-13	Sequence 13, Appl	223	29	54.7	2348	6	US-11-124-367A-304	Sequence 304, App
151	29	54.7	306	7	US-11-187-687-14	Sequence 14, Appl	224	29	54.7	3256	7	US-11-124-367A-432	Sequence 432, App
152	29	54.7	306	7	US-11-187-687-15	Sequence 15, Appl	225	29	54.7	3256	7	US-11-087-099-10885	Sequence 10885, A
153	29	54.7	306	7	US-11-187-687-16	Sequence 16, Appl	226	29	54.7	3475	6	US-10-467-657-2882	Sequence 2882, App
154	29	54.7	306	7	US-11-187-687-17	Sequence 17, Appl	227	29	54.7	65	6	US-10-467-657-2882	Sequence 10132, A
155	29	54.7	306	7	US-11-187-687-18	Sequence 18, Appl	228	29	54.7	71	7	US-11-079-463-10192	Sequence 175, App
156	29	54.7	306	7	US-11-187-687-19	Sequence 19, Appl	229	29	54.7	86	6	US-10-475-075-175	Sequence 460, App
157	29	54.7	306	7	US-11-187-687-20	Sequence 20, Appl	230	29	54.7	86	6	US-10-475-075-460	Sequence 80, Appl
158	29	54.7	306	7	US-11-002-387-35	Sequence 35, Appl	231	29	54.7	109	7	US-11-077-619-80	Sequence 47, Appl
159	29	54.7	306	7	US-11-002-387-37	Sequence 37, Appl	232	29	54.7	151	6	US-10-853-807A-47	Sequence 7190, App
160	29	54.7	306	7	US-11-002-387-38	Sequence 38, Appl	233	29	54.7	181	7	US-11-087-099-7190	Sequence 17640, A
161	29	54.7	306	7	US-11-002-387-39	Sequence 39, Appl	234	29	54.7	181	7	US-11-188-298-17640	Sequence 23128, A
162	29	54.7	306	7	US-11-002-387-40	Sequence 40, Appl	235	29	54.7	187	7	US-11-096-568A-23128	Sequence 23127, A
163	29	54.7	306	7	US-11-002-387-41	Sequence 41, Appl	236	29	54.7	189	7	US-11-096-568A-23127	Sequence 5478, App
164	29	54.7	306	7	US-11-002-387-42	Sequence 42, Appl	237	29	54.7	189	7	US-11-079-463-5478	Sequence 3495, App
165	29	54.7	306	7	US-11-002-387-43	Sequence 43, Appl	238	29	54.7	200	7	US-11-087-099-3495	Sequence 3294, App
166	29	54.7	306	7	US-11-002-387-44	Sequence 44, Appl	239	29	54.7	200	7	US-11-188-298-3294	Sequence 9810, App
167	29	54.7	306	7	US-11-002-387-45	Sequence 45, Appl	240	29	54.7	220	7	US-11-087-099-9810	Sequence 9066, App
168	29	54.7	306	7	US-11-002-387-46	Sequence 46, Appl	241	29	54.7	220	7	US-11-188-298-9066	Sequence 6620, App
169	29	54.7	306	7	US-11-002-387-47	Sequence 47, Appl	242	29	54.7	231	7	US-11-188-298-6620	Sequence 21886, A
170	29	54.7	306	7	US-11-002-387-48	Sequence 48, Appl	243	29	54.7	231	7	US-11-188-298-21886	Sequence 728, App
171	29	54.7	306	7	US-11-002-387-49	Sequence 49, Appl	244	29	54.7	249	6	US-10-330-773-728	

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OM protein - protein search, using sw model

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(without alignments)
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Title: US-10-091-135-13

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Searched: 217505 seqs, 42489236 residues

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	37	69.8	206	6	US-10-498-026-80
4	36	67.9	136	7	US-11-156-084-324
5	36	67.9	244	7	US-11-156-084-218
6	35	66.0	749	7	US-11-079-463-5493
7	35	66.0	4868	7	US-11-044-111-24
8	34	64.2	215	6	US-10-793-626-828
9	34	64.2	407	7	US-11-079-463-8587
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12	33	62.3	399	7	US-11-188-298-5973
13	33	62.3	465	7	US-11-156-084-101
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15	33	62.3	2353	7	US-11-097-728-6
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23	32	60.4	342	7	US-11-096-568A-10715
24	32	60.4	356	7	US-11-096-568A-10714
25	32	60.4	606	7	US-11-079-463-9950
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29	31	58.5	281	7	US-11-144-833-14
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62	30	56.6	382	7	US-11-203-526-4
63	30	56.6	389	7	US-11-087-099-2227
64	30	56.6	394	7	US-11-203-526-6
65	30	56.6	398	7	US-11-072-512-3388
66	30	56.6	416	7	US-11-096-568A-6311
67	30	56.6	442	7	US-11-096-568A-19513
68	30	56.6	450	7	US-11-096-568A-6310
69	30	56.6	453	6	US-10-466-794A-5
70	30	56.6	457	7	US-11-096-568A-19512
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75	30	56.6	554	7	US-11-096-568A-28079
76	30	56.6	579	7	US-11-096-568A-28078
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84	29	54.7	129	6	US-10-467-657-4354
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93	29	54.7	258	7	US-11-096-568A-3312
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102	33	62.3	326	4	US-10-282-122A-72088	Sequence 72088, A	175	32	60.4	467	4	US-10-424-599-169015	Sequence 169015,
103	33	62.3	348	4	US-10-221-625-7	Sequence 7, Appl1	176	32	60.4	482	5	US-10-732-923-22822	Sequence 22822, A
104	33	62.3	377	5	US-10-741-849-7077	Sequence 7077, Ap	178	32	60.4	501	4	US-10-389-566-2058	Sequence 2058, Ap
105	33	62.3	378	6	US-11-097-143-27192	Sequence 27192, A	179	32	60.4	515	4	US-10-424-599-276081	Sequence 276081,
106	33	62.3	420	3	US-09-773-517-9	Sequence 9, Appl1	179	32	60.4	521	4	US-10-282-122A-70198	Sequence 70198, A
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108	33	62.3	420	3	US-09-849-868-9	Sequence 9, Appl1	181	32	60.4	521	4	US-10-732-923-22820	Sequence 22820, A
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116	33	62.3	533	4	US-10-424-599-215311	Sequence 215311,	189	32	60.4	521	4	US-10-732-923-22820	Sequence 22820, A
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OM protein - protein search, using sw model

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Listing first 1000 summaries

Database : Published Applications AA Main:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	53	100.0	209	3	US-09-957-808A-22
6	53	100.0	210	4	US-10-001-245-214
7	49	92.5	204	3	US-09-847-208-162
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9	49	92.5	204	4	US-10-091-135-63
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11	47	88.7	204	4	US-10-091-135-64
12	47	88.7	227	4	US-10-091-135-81
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14	47	88.7	227	5	US-10-809-689-82
15	46	86.8	204	3	US-09-847-208-163
16	46	86.8	204	3	US-09-847-208-166
17	46	86.8	204	4	US-10-091-135-66
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19	44	83.0	354	4	US-10-289-762-317
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25	37	69.8	206	5	US-10-809-689-86
26	37	69.8	674	6	US-11-097-143-13863
27	37	69.8	1425	5	US-10-450-763-53703

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59	34	64.2	150	4	US-10-425-115-350457	Sequence 350457, A
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63	34	64.2	304	4	US-10-289-762-541	Sequence 541, App
64	34	64.2	311	5	US-10-501-282-1192	Sequence 1192, Ap
65	34	64.2	314	5	US-10-501-282-1194	Sequence 1194, Ap
66	34	64.2	386	4	US-10-424-599-170944	Sequence 170944, A
67	34	64.2	387	4	US-10-282-122A-52400	Sequence 52400, A
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70	34	64.2	517	4	US-10-425-114-55637	Sequence 55637, A
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88	33	62.3	129	3	US-09-795-668-33	Sequence 33, Appl1
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103	33	62.3	639	2	US-08-411-295F-167	Sequence 167, App	176	32	60.4	269	2	US-09-270-767-54772	Sequence 54772, A
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108	33	62.3	650	2	US-08-411-295F-106	Sequence 106, App	181	32	60.4	533	2	US-08-726-214-18	Sequence 4365, Ap
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110	33	62.3	658	2	US-08-467-602-358	Sequence 358, App	183	32	60.4	1090	2	US-08-307-896-3	Sequence 4, Appl
111	33	62.3	658	2	US-08-467-602-388	Sequence 388, App	184	32	60.4	1090	2	US-08-726-214-4	Sequence 3, Appl
112	33	62.3	658	2	US-08-411-295F-231	Sequence 231, App	185	32	60.4	1090	2	US-08-245-039-3	Sequence 3, Appl
113	33	62.3	660	2	US-08-411-295F-294	Sequence 294, App	186	32	60.4	1090	2	PCT-US93-11808-3	Sequence 3, Appl
114	33	62.3	660	2	US-08-467-602-264	Sequence 264, App	187	31	58.5	79	2	US-09-248-796A-26366	Sequence 26366, A
115	33	62.3	660	2	US-08-411-295F-190	Sequence 190, App	188	31	58.5	98	2	US-08-123-934A-12	Sequence 12, Appl
116	33	62.3	669	2	US-08-467-602-344	Sequence 344, App	189	31	58.5	98	2	US-08-874-628-12	Sequence 12, Appl
117	33	62.3	669	2	US-08-411-295F-270	Sequence 270, App	190	31	58.5	98	2	US-09-874-628-12	Sequence 12, Appl
118	33	62.3	673	2	US-08-467-602-220	Sequence 220, App	191	31	58.5	142	2	PCT-US94-10080-12	Sequence 7201, Ap
119	33	62.3	673	2	US-08-467-602-283	Sequence 283, App	192	31	58.5	166	2	US-09-641-976-7201	Sequence 8056, Ap
120	33	62.3	673	2	US-08-411-295F-146	Sequence 146, App	193	31	58.5	193	2	US-09-949-016-8056	Sequence 33693, A
121	33	62.3	684	2	US-08-411-295F-209	Sequence 209, App	194	31	58.5	193	2	US-09-270-767-33693	Sequence 48910, A
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126	33	62.3	707	2	US-09-538-093-303	Sequence 303, App	199	31	58.5	261	2	US-09-107-532A-6012	Sequence 41672, A
127	33	62.3	707	2	US-08-467-602-262	Sequence 262, App	200	31	58.5	261	2	US-09-270-767-41672	Sequence 41676, A
128	33	62.3	707	2	US-08-411-295F-188	Sequence 188, App	201	31	58.5	277	2	US-09-270-767-41676	Sequence 24, Appl
129	33	62.3	818	2	US-08-470-335-234	Sequence 234, App	202	31	58.5	277	2	US-09-198-452A-24	Sequence 14, Appl
130	33	62.3	818	2	US-08-467-602-321	Sequence 321, App	203	31	58.5	281	2	US-09-125-031C-14	Sequence 3644, Ap
131	33	62.3	818	2	US-08-411-295F-247	Sequence 247, App	204	31	58.5	287	2	US-09-583-110-3644	Sequence 5097, Ap
132	33	62.3	841	2	US-08-467-602-327	Sequence 327, App	205	31	58.5	293	2	US-09-107-433-5097	Sequence 16, Appl
133	33	62.3	841	2	US-08-411-295F-253	Sequence 253, App	206	31	58.5	300	2	US-08-158-735A-16	Sequence 17, Appl
134	33	62.3	852	2	US-08-470-335-248	Sequence 248, App	207	31	58.5	311	2	US-08-158-735A-17	Sequence 331, App
135	33	62.3	852	2	US-08-467-602-300	Sequence 300, App	208	31	58.5	311	2	US-09-198-452A-331	Sequence 316, App
136	33	62.3	852	2	US-08-467-602-363	Sequence 363, App	209	31	58.5	363	1	US-09-438-185A-316	Sequence 20, Appl
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139	33	62.3	865	2	US-08-470-335-235	Sequence 235, App	212	31	58.5	403	2	US-09-470-526-2	Sequence 2, Appl
140	33	62.3	865	2	US-08-467-602-322	Sequence 322, App	213	31	58.5	423	2	US-09-107-532A-6847	Sequence 6847, Ap
141	33	62.3	865	2	US-08-411-295F-248	Sequence 248, App	214	31	58.5	424	1	US-08-247-908A-11	Sequence 11, Appl
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144	33	62.3	875	2	US-08-411-295F-232	Sequence 232, App	217	31	58.5	424	1	PCT-US94-05290-11	Sequence 11, Appl
145	33	62.3	875	2	US-08-411-295F-295	Sequence 295, App	218	31	58.5	448	2	US-09-134-001C-3055	Sequence 3055, Ap
146	33	62.3	886	2	US-08-467-602-342	Sequence 342, App	219	31	58.5	478	2	US-09-710-279-1728	Sequence 1728, Ap
147	33	62.3	886	2	US-08-411-295F-268	Sequence 268, App	220	31	58.5	481	2	US-09-134-000C-4712	Sequence 4712, Ap
148	33	62.3	888	2	US-08-467-602-325	Sequence 325, App	221	31	58.5	481	2	US-08-830-230A-546	Sequence 546, App
149	33	62.3	888	2	US-08-411-295F-251	Sequence 251, App	222	31	58.5	493	1	US-08-341-916-2	Sequence 2, Appl
150	33	62.3	899	2	US-08-470-335-249	Sequence 249, App	223	31	58.5	493	1	US-08-805-166-2	Sequence 2, Appl
151	33	62.3	899	2	US-08-467-602-301	Sequence 301, App	224	31	58.5	493	1	US-08-805-169-2	Sequence 2, Appl
152	33	62.3	899	2	US-08-467-602-364	Sequence 364, App	225	31	58.5	493	1	US-08-957-365-2	Sequence 2, Appl
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155	33	62.3	909	2	US-08-467-602-348	Sequence 348, App	228	31	58.5	493	2	US-09-069-228-2	Sequence 2, Appl
156	33	62.3	922	2	US-08-411-295F-274	Sequence 274, App	229	31	58.5	493	2	US-09-742-684A-12	Sequence 12, Appl
157	33	62.3	922	2	US-08-467-602-304	Sequence 304, App	230	31	58.5	494	2	US-09-949-016-10396	Sequence 10396, A
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159	33	62.3	922	2	US-08-411-295F-230	Sequence 230, App	232	31	58.5	500	2	US-08-158-735A-2	Sequence 2, Appl
160	33	62.3	933	2	US-08-411-295F-293	Sequence 293, App	233	31	58.5	501	1	US-08-158-735A-2	Sequence 2, Appl
161	33	62.3	933	2	US-08-467-602-343	Sequence 343, App	234	31	58.5	501	1	US-08-149-105-15	Sequence 15, Appl
162	33	62.3	956	2	US-08-411-295F-269	Sequence 269, App	235	31	58.5	501	1	US-08-149-105-17	Sequence 17, Appl
163	33	62.3	956	2	US-08-467-602-346	Sequence 346, App	236	31	58.5	501	1	US-08-317-847-15	Sequence 15, Appl
164	33	62.3	956	2	US-08-411-295F-272	Sequence 272, App	237	31	58.5	501	1	US-08-317-847-17	Sequence 17, Appl
165	33	62.3	2308	1	US-08-015-973-1	Sequence 1, Appl	238	31	58.5	502	1	US-09-949-016-9766	Sequence 9766, Ap
166	33	62.3	2308	1	US-08-448-164-1	Sequence 1, Appl	239	31	58.5	502	1	US-08-481-317A-8	Sequence 8, Appl
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168	33	62.3	2314	2	US-10-000-954-2	Sequence 2, Appl	241	31	58.5	502	2	US-09-395-115-18	Sequence 18, Appl
169	32	60.4	177	2	US-09-816-703A-2	Sequence 2, Appl	242	31	58.5	502	2	US-08-123-934A-4	Sequence 4, Appl
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					Sequence 1658, Ap							US-08-448-371A-8	Sequence 8, Appl

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:24:04 ; Search time 13.9583 Seconds
(without alignments)
59.230 Million cell updates/sec

Title: US-10-091-135-13

Perfect score: 53

Sequence: 1 FKNEELYQTK 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : Issued Patents AA:*

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5: /cgn2_6/ptodata/1/1aa/RE COMB.pep:*

6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	49	92.5	204	1	US-09-130-287-1
3	47	88.7	204	1	US-08-419-414-9
4	47	88.7	204	1	US-08-614-935-2
5	47	88.7	204	2	US-09-130-287-2
6	47	88.7	227	2	US-09-541-759-6
7	44	83.0	354	2	US-09-198-452A-317
8	44	83.0	354	2	US-09-438-185A-305
9	39	73.6	950	2	US-09-248-796A-15047
10	37	69.8	4866	2	US-09-424-783-2
11	37	69.8	4872	2	US-09-424-783-3
12	36	67.9	1115	2	US-09-976-594-893
13	36	67.9	3696	2	US-09-134-001C-5080
14	35	66.0	798	2	US-10-101-464A-926
15	34	64.2	26	1	US-08-563-892A-7
16	34	64.2	26	2	US-09-366-212A-7
17	34	64.2	215	2	US-09-902-540-15254
18	34	64.2	257	2	US-09-710-279-828
19	34	64.2	224	2	US-09-134-001C-5295
20	34	64.2	204	2	US-09-198-452A-541
21	34	64.2	409	2	US-09-438-185A-503
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26	33	62.3	63	2	US-09-020-880-7
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40	33	62.3	300	2	US-09-102-716-4	Sequence 4, Appli
41	33	62.3	317	2	US-09-270-767-41609	Sequence 41609, A
42	33	62.3	352	2	US-08-467-602-239	Sequence 239, App
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44	33	62.3	375	2	US-08-467-602-242	Sequence 242, App
45	33	62.3	375	2	US-08-411-295F-168	Sequence 168, App
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50	33	62.3	401	2	US-09-248-796A-15983	Sequence 15983, A
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53	33	62.3	409	2	US-08-411-295F-147	Sequence 147, App
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56	33	62.3	420	1	US-08-456-201-29	Sequence 29, Appl
57	33	62.3	420	1	US-08-456-241-29	Sequence 29, Appl
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63	33	62.3	443	2	US-08-467-602-263	Sequence 263, App
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65	33	62.3	450	2	US-08-467-602-195	Sequence 195, App
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67	33	62.3	474	2	US-08-467-602-190	Sequence 190, App
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71	33	62.3	569	2	US-08-467-602-237	Sequence 237, App
72	33	62.3	569	2	US-08-411-295F-163	Sequence 163, App
73	33	62.3	592	2	US-08-467-602-243	Sequence 243, App
74	33	62.3	592	2	US-08-411-295F-169	Sequence 169, App
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76	33	62.3	601	2	US-08-467-602-323	Sequence 323, App
77	33	62.3	601	2	US-08-411-295F-249	Sequence 249, App
78	33	62.3	603	2	US-08-467-602-216	Sequence 216, App
79	33	62.3	603	2	US-08-467-602-279	Sequence 279, App
80	33	62.3	603	2	US-08-411-295F-142	Sequence 142, App
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84	33	62.3	623	2	US-09-107-532A-4726	Sequence 4726, Ap
85	33	62.3	624	2	US-08-467-602-326	Sequence 326, App
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87	33	62.3	626	2	US-08-467-602-222	Sequence 222, App
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98	33	62.3	637	1	US-08-456-241-28	Sequence 28, Appl
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100	33	62.3	637	2	US-08-411-295F-184	Sequence 184, App

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106	35	66.0	482	2	Q61G01_CAEBR	Q61G01 caenorhabdi	179	34	64.2	404	2	Q64RQ0_BACFR	Q92850 bacteroides
107	35	66.0	485	2	Q9XVK0_CAEBL	Q9XVK0 caenorhabdi	180	34	64.2	414	2	Q7Q6H1_ANOGR	Q7Q6H1 anopheles g
108	35	66.0	492	2	Q4HN36_CAMLA	Q4HN36 campylobact	181	34	64.2	416	2	Q9C2D6_NEUCR	Q9C2D6 neurospora
109	35	66.0	496	2	Q41104_GIBZE	Q41104 gibberella	182	34	64.2	432	2	Q41BJ6_GIBZE	Q41BJ6 gibberella
110	35	66.0	502	1	PTL_LISIN	PTL_LISIN listeria in	183	34	64.2	443	2	Q5CUN2_CRYPV	Q5CUN2 cryptospori
111	35	66.0	572	1	PTL_LISMO	PTL_LISMO listeria in	184	34	64.2	443	2	Q5CPC4_CRYHO	Q5CPC4 cryptospori
112	35	66.0	572	1	Q72IG3_LISMF	Q72IG3 listeria mo	185	34	64.2	448	2	Q81JUC4_PLAF7	Q81JUC4 plasmodium
113	35	66.0	578	2	Q81S24_PLAF7	Q81S24 listeria mo	186	34	64.2	484	2	Q9QXX8_MOUSE	Q9QXX8 m nuclear f
114	35	66.0	599	1	PARE_BORBU	PARE_BORBU borrelia bu	187	34	64.2	485	1	RNF8_HUMAN	Q76064 homo sapien
115	35	66.0	599	2	Q662X6_BORCA	Q662X6 borrelia ga	188	34	64.2	485	2	Q53H16_HUMAN	Q53H16 homo sapien
116	35	66.0	630	2	Q8SQV0_ENCCU	Q8SQV0 encephalito	189	34	64.2	485	2	Q5NKM5_HUMAN	Q5NKM5 homo sapien
117	35	66.0	742	2	Q5LCK8_BACFN	Q5LCK8 bacteroides	190	34	64.2	486	2	Q5R412_PONPY	Q5R412 pongo pygma
118	35	66.0	742	2	Q64TQ7_BACFR	Q64TQ7 bacteroides	191	34	64.2	487	2	Q52SAS_ORYSA	Q52SAS oryza sativ
119	35	66.0	750	2	Q91D04_9VIRU	Q91D04 torque teno	192	34	64.2	488	1	RNF8_MOUSE	Q8V556 mus musculu
120	35	66.0	859	2	Q4YQV1_PLABE	Q4YQV1 mycoplasma	193	34	64.2	488	2	Q4FJV7_MOUSE	Q4FJV7 mus musculu
121	35	66.0	897	2	Q98QG9_MYCPU	Q98QG9 mycoplasma	194	34	64.2	511	2	Q4YUD4_PLABE	Q4YUD4 plasmodium
122	35	66.0	899	2	Q4YXB5_PLABE	Q4YXB5 plasmodium	195	34	64.2	512	2	Q4YSZ6_PLABE	Q4YSZ6 plasmodium
123	35	66.0	906	2	Q7RQF1_PLAYO	Q7RQF1 plasmodium	196	34	64.2	552	2	Q8VZC8_ARATH	Q8VZC8 arabidopsis
124	35	66.0	911	2	Q7RQJ2_PLAYO	Q7RQJ2 plasmodium	197	34	64.2	556	2	Q97046_HAURO	Q97046 halocynthia
125	35	66.0	962	2	Q6BGL0_PARTE	Q6BGL0 parameseli	198	34	64.2	565	2	Q72W94_LEPIC	Q72W94 leptospira
126	35	66.0	982	2	Q7BJR4_ANOGR	Q7BJR4 anopheles g	199	34	64.2	565	2	Q8F9Y8_LEPIN	Q8F9Y8 leptospira
127	35	66.0	1033	2	Q81BB8_PLAF7	Q81BB8 plasmodium	200	34	64.2	568	2	Q7RMU3_PLAYO	Q7RMU3 plasmodium
128	35	66.0	1228	2	Q9U4H2_DROME	Q9U4H2 drosophila	201	34	64.2	575	2	Q54FM8_DICDI	Q54FM8 dictyosteli
129	35	66.0	1268	2	Q5CVS0_CRYPV	Q5CVS0 cryptospori	202	34	64.2	590	2	Q4YIT3_PLABE	Q4YIT3 plasmodium
130	35	66.0	1268	2	Q5CJQ8_CRYHO	Q5CJQ8 cryptospori	203	34	64.2	620	1	ORC2_YEAST	P32833 saccharomyc
131	35	66.0	1317	2	Q5CVF5_CRYPV	Q5CVF5 cryptospori	204	34	64.2	628	2	Q97243_PLAF7	Q97243 plasmodium
132	35	66.0	1318	2	Q5CHP5_CRYHO	Q5CHP5 cryptospori	205	34	64.2	643	2	Q54Y78_DICDI	Q54Y78 dictyosteli
133	35	66.0	1440	2	Q4RPR0_TETNG	Q4RPR0 tetraodon n	206	34	64.2	656	2	Q6KH15_MYCWO	Q6KH15 mycoplasma
134	35	66.0	1583	2	Q6DNE6_9CYAN	Q6DNE6 lyngbya maj	207	34	64.2	690	1	Y173_UREPA	Q9P9X0 ureaplasma
135	35	66.0	1698	2	Q9V815_DROME	Q9V815 drosophila	208	34	64.2	749	2	Q6A0Z1_MOUSE	Q6A0Z1 mus musculu
136	35	66.0	1701	2	Q9V816_DROME	Q9V816 drosophila	209	34	64.2	778	2	Q4YNZ9_PLABE	Q4YNZ9 plasmodium
137	35	66.0	1712	2	Q6LFW0_PLAF7	Q6LFW0 plasmodium	210	34	64.2	829	2	Q54DN9_DICDI	Q54DN9 dictyosteli
138	35	66.0	1781	2	Q7PDN3_PLAYO	Q7PDN3 plasmodium	211	34	64.2	847	2	Q4PFJ1_USTMA	Q4PFJ1 ustilago ma
139	35	66.0	1922	2	Q8MLH7_DROME	Q8MLH7 drosophila	212	34	64.2	907	2	Q54J31_DICDI	Q54J31 dictyosteli
140	35	66.0	1923	2	Q6ANF2_DROME	Q6ANF2 drosophila	213	34	64.2	908	2	Q6CML0_KULJA	Q6CML0 kluyveromyc
141	35	66.0	4097	2	Q7RG07_PLAYO	Q7RG07 plasmodium	214	34	64.2	1040	2	Q4YNV3_PLABE	Q4YNV3 plasmodium
142	35	66.0	4869	2	Q90985_CHICK	Q90985 gallus gall	215	34	64.2	1243	2	Q4Z6H8_PLABE	Q4Z6H8 plasmodium
143	35	66.0	6118	2	Q81396_PLAF7	Q81396 plasmodium	216	34	64.2	1370	2	Q8AB44_BACTN	Q8AB44 bacteroides
144	34	64.2	109	2	Q5JLE4_ORYSA	Q5JLE4 oryza sativ	217	34	64.2	1481	2	Q81BB3_PLAF7	Q81BB3 plasmodium
145	34	64.2	121	1	RL7A_THEAC	RL7A thermoplasm	218	34	64.2	2779	2	Q81LH0_PLAF7	Q81LH0 plasmodium
146	34	64.2	121	1	RL7A_THEAO	RL7A thermoplasm	219	34	64.2	3394	2	Q77384_PLAF7	Q77384 plasmodium
147	34	64.2	138	2	Q5WHE0_BACSK	Q5WHE0 bacillus ci	220	34	64.2	4507	2	Q7RFG7_PLAYO	Q7RFG7 plasmodium
148	34	64.2	152	2	Q5JF25_PYRKO	Q5JF25 pyrococcus	221	34	64.2	10578	2	Q81SF5_CABEL	Q81SF5 caenorhabdi
149	34	64.2	173	1	CD3D_MOUSE	P04235 mus musculu	222	34	64.2	18519	2	Q81SF6_CABEL	Q81SF6 caenorhabdi
150	34	64.2	173	1	CD3D_MOUSE	P19377 rattus norv	223	34	64.2	18534	2	Q81SF7_CABEL	Q81SF7 caenorhabdi
151	34	64.2	173	1	Q6P5F1_MOUSE	Q6P5F1 mus musculu	224	35	63.2	377	2	Q9WHG3_HPV18	Q9WHG3 human papil
152	34	64.2	191	2	P70895_BORCA	P70895 borrelia ga	225	33	62.3	59	2	Q54JZ5_DICDI	Q54JZ5 dictyosteli
153	34	64.2	192	2	Q9XGJ9_GNEG	Q9XGJ9 gnetum gnet	226	33	62.3	61	2	Q5ZSE4_LIEGPH	Q5ZSE4 wolbachia e
154	34	64.2	201	2	Q7QM18_ANOGR	Q7QM18 anopheles g	227	33	62.3	78	2	Q5ZSE4_LIEGPH	P59527 buchnera ap
155	34	64.2	203	2	Q4L9L1_STAHI	Q4L9L1 staphylococ	228	33	62.3	109	1	THIO_BUCBP	Q52517 legionella
156	34	64.2	215	2	Q5HRH5_STAHO	Q5HRH5 staphylococ	229	33	62.3	113	2	Q4Z5W7_PLABE	Q4Z5W7 plasmodium
157	34	64.2	215	2	Q8CQ68_STAHP	Q8CQ68 staphylococ	230	33	62.3	116	2	Q823C0_CHLCV	Q823C0 chlamydropi
158	34	64.2	233	2	Q7RR04_PLAYO	Q7RR04 plasmodium	231	33	62.3	125	2	Q515Y0_ENTHI	Q515Y0 entamoeba h
159	34	64.2	233	2	Q4YFA0_PLABE	Q4YFA0 plasmodium	232	33	62.3	126	2	Q8SR06_ENCCU	Q8SR06 encephalito
160	34	64.2	245	2	Q4Y888_PLACH	Q4Y888 plasmodium	233	33	62.3	141	2	Q8GCI4_BACCE	Q8GCI4 bacillus ce
161	34	64.2	246	2	Q7TU63_PROMP	Q7TU63 prochloroco	234	33	62.3	145	2	Q64Q27_BACFR	Q64Q27 bacteroides
162	34	64.2	249	2	Q9CV69_MOUSE	Q9CV69 mus musculu	235	33	62.3	148	2	Q4X1Z3_PLACH	Q4X1Z3 plasmodium
163	34	64.2	268	2	Q5CXU9_CRYPV	Q5CXU9 cryptospori	236	33	62.3	148	2	Q8ETE0_OCEIH	Q8ETE0 oceanobacil
164	34	64.2	295	2	Q9USC1_CABEL	Q9USC1 caenorhabdi	237	33	62.3	149	2	Q84SB9_ORYSA	Q84SB9 oryza sativ
165	34	64.2	296	2	Q96253_SULTO	Q96253 sulfolobus	238	33	62.3	162	2	Q6MTI2_MYCMS	Q6MTI2 mycoplasma
166	34	64.2	309	2	Q4RJL1_TETNG	Q4RJL1 tetraodon n	239	33	62.3	168	2	Q5A431_CANAL	Q5A431 candida alb
167	34	64.2	310	2	Q7R4N4_GIALA	Q7R4N4 giardia lam	240	33	62.3	168	2	Q5DHK4_SCHJA	Q5DHK4 schistosoma
168	34	64.2	345	2	Q4YQT9_PLABE	Q4YQT9 plasmodium	241	33	62.3	170	2	Q8RAD9_THETN	Q8RAD9 thermoanaer
169	34	64.2	367	2	Q4YSU9_PLABE	Q4YSU9 plasmodium	242	33	62.3	183	2	Q64WJ5_BACFR	Q64WJ5 bacteroides
170	34	64.2	370	2	Q9K5S4_BACHD	Q9K5S4 bacillus ha	243	33	62.3	189	2	Q58WX6_ORENI	Q58WX6 oreochromis
171	34	64.2	377	2	Q9LNU7_ARATH	Q9LNU7 arabidopsis	244	33	62.3	209	2	Q8RRR7_HELPY	Q8RRR7 helicobacte
172	34	64.2	378	2	Q9HJF4_THEAC	Q9HJF4 thermoplasm	245	33	62.3	209	2	Q8RRS2_HELPY	Q8RRS2 helicobacte
173	34	64.2	386	1	HRCA_CHLAB	HRCA chlamydropi	246	33	62.3	214	2	Q8RRR6_HELPY	Q8RRR6 helicobacte
174	34	64.2	386	1	HRCA_CHLCV	HRCA chlamydropi	247	33	62.3	214	2	Q8RRR8_HELPY	Q8RRR8 helicobacte
175	34	64.2	391	2	Q5LBA3_BACFN	Q5LBA3 bacteroides	248	33	62.3	228	2	Q6ONC3_CABER	Q6ONC3 caenorhabdi
176	34	64.2	392	1	HRCA_CHLMU	P54306 chlamydia m	249	33	62.3	231	2	Q4XNG9_PLACH	Q4XNG9 plasmodium
177	34	64.2	392	1	HRCA_CHLTR	P36426 chlamydia t	250	33	62.3	241	2	Q6MKV7_DBDEA	Q6MKV7 bdellovibri

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:16:43 ; Search time 105.417 Seconds
(without alignments)
66.928 Million cell updates/sec

Title: US-10-091-135-13
Perfect score: 53
Sequence: 1 FKNEELYQTK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	92.5	204	1 VA5_VESFL	P35783 vespula fla
2	49	92.5	204	1 VA5_VESMC	P35760 vespula mac
3	47	88.7	227	1 VA5_VESVU	Q05110 vespula vul
4	46	86.8	204	1 VA5_VESGE	P35784 vespula ger
5	46	86.8	204	1 VA5_VESPE	P35785 vespula pen
6	44	83.0	346	2 Q9K265_CHLPN	Q9K265 chlamydia p
7	44	83.0	346	2 Q928N5_CHLPN	Q928N5 chlamydia p
8	41	77.4	90	2 Q6JRM6_9MOLU	Q6JRM6 beet leafh
9	41	77.4	90	2 Q6JRM5_9MOLU	Q6JRM5 beet leafh
10	41	77.4	416	2 Q8I366_PLAF7	Q8I366 plasmodium
11	40	75.5	385	2 Q4MIF9_BACCE	Q4MIF9 bacillus ce
12	40	75.5	838	2 Q75G12_LEPIC	Q75G12 leptospira
13	40	75.5	3165	2 Q8IJL8_PLAF7	Q8IJL8 plasmodium
14	39	73.6	123	2 Q4MHP6_BACCE	Q4MHP6 bacillus ce
15	39	73.6	245	2 Q8I1D1_BACCR	Q8I1D1 bacillus ce
16	39	73.6	246	2 Q6HIL8_BACHK	Q6HIL8 bacillus th
17	39	73.6	248	2 Q737X3_BACCI	Q737X3 bacillus ce
18	39	73.6	248	2 Q63B91_BACCC	Q63B91 bacillus ce
19	39	73.6	518	2 Q5TVD2_ANOGA	Q5TVD2 anophles g
20	39	73.6	1235	2 Q5A7S2_CANAL	Q5A7S2 candida alb
21	38	71.7	343	2 Q5L611_CHLAB	Q5L611 chlamydia
22	38	71.7	547	2 Q8MYK6_9BILA	Q8MYK6 priapulid c
23	38	71.7	1386	2 Q5A4S8_DICDI	Q5A4S8 dictyosteli
24	38	71.7	1422	2 Q5A4V1_DICDI	Q5A4V1 dictyosteli
25	38	71.7	1437	2 Q9GQ51_DICDI	Q9GQ51 dictyosteli
26	37	69.8	178	2 Q5GHG3_CANOL	Q5GHG3 candida ole
27	37	69.8	158	2 Q4HF29_CAMCO	Q4HF29 campylobact
28	37	69.8	206	1 VA5_VESVI	P35787 vespula vid
29	37	69.8	299	2 Q7Q6J3_ANOGA	Q7Q6J3 anophles g
30	37	69.8	416	2 Q96144_PLAF7	Q96144 plasmodium
31	37	69.8	454	2 Q9QY91_MOUSE	Q9QY91 mus musculu

32	37	69.8	674	2	Q9VC92_DROME	Q9VC92 drosophila
33	37	69.8	721	2	Q511V1_ENTHI	Q511V1 entamoeba h
34	37	69.8	791	2	Q5CY49_CRYPV	Q5CY49 cryptospori
35	37	69.8	791	2	Q5CN15_CRYHO	Q5CN15 cryptospori
36	37	69.8	838	2	Q8EY56_LEPIN	Q8EY56 leptospira
37	37	69.8	1615	2	Q6FK87_CANGA	Q6FK87 candida gla
38	37	69.8	1809	2	Q15892_TETHH	Q15892 tetrahymena
39	37	69.8	2627	2	Q4IQB1_GIBZE	Q4IQB1 gibberella
40	37	69.8	3009	2	Q7RG60_PLAYO	Q7RG60 plasmodium
41	37	69.8	4859	2	Q95201_MUSVI	Q95201 mustela vis
42	37	69.8	4859	2	Q7M2T9_9CARN	Q7M2T9 mustela sp.
43	37	69.8	4870	1	RYR3_HUMAN	Q15413 homo sapien
44	37	69.8	4872	2	Q9TS53_RABIT	Q9TS53 oryctolagus
45	36	67.9	109	2	Q8CV63_OCEIH	Q8CV63 oceanobacil
46	36	67.9	136	2	Q9WMN9_ANASP	Q9WMN9 anabaena sp
47	36	67.9	244	2	Q8Z078_ANASP	Q8Z078 anabaena sp
48	36	67.9	246	2	Q6HYL3_BACAN	Q6HYL3 bacillus an
49	36	67.9	248	2	Q810D6_BACAN	Q810D6 bacillus an
50	36	67.9	310	2	Q9BV59_HUMAN	Q9BV59 homo sapien
51	36	67.9	387	2	Q9FPY6_UREPA	Q9FPY6 ureaplasma
52	36	67.9	396	2	Q6NZC1_MOUSE	Q6NZC1 mus musculu
53	36	67.9	439	1	RNBP6_MOUSE	Q8BIV3 mus musculu
54	36	67.9	591	2	Q6K2L3_ORYSA	Q6K2L3 oryza sativ
55	36	67.9	798	2	Q7TN23_MOUSE	Q7TN23 mus musculu
56	36	67.9	964	2	Q6BG56_PARTE	Q6BG56 paramescium
57	36	67.9	995	2	Q54PU7_DICDI	Q54PU7 dictyosteli
58	36	67.9	1084	2	Q4R8T7_MACEFA	Q4R8T7 macaca faec
59	36	67.9	1094	2	Q804V4_XENLA	Q804V4 xenopus lae
60	36	67.9	1094	2	Q7ZT67_XENLA	Q7ZT67 xenopus lae
61	36	67.9	1097	1	IMB3_HUMAN	Q00410 homo sapien
62	36	67.9	1097	1	IMB3_MOUSE	Q8BKC5 mus musculu
63	36	67.9	1097	1	Q5T578_HUMAN	Q5T578 homo sapien
64	36	67.9	1098	2	Q68FK3_XENLA	Q68FK3 xenopus lae
65	36	67.9	1105	1	RNBP6_HUMAN	Q60518 homo sapien
66	36	67.9	1105	2	Q5T7X4_HUMAN	Q5T7X4 homo sapien
67	36	67.9	1107	2	Q7ZT18_XENLA	Q7ZT18 xenopus lae
68	36	67.9	1115	2	Q86XC7_HUMAN	Q86XC7 homo sapien
69	36	67.9	1204	2	Q4Y6X5_PLACH	Q4Y6X5 plasmodium
70	36	67.9	1284	2	Q61VN1_CABBR	Q61VN1 caenorhabdi
71	36	67.9	2282	2	Q9NK56_DROME	Q9NK56 drosophila
72	36	67.9	2501	2	Q4UIN5_THEAN	Q4UIN5 theileria a
73	36	67.9	2668	2	Q8IE42_PLAF7	Q8IE42 plasmodium
74	36	67.9	3692	2	Q5HNF3_STAEQ	Q5HNF3 staphylococ
75	36	67.9	3692	2	Q8CN99_STAEP	Q8CN99 staphylococ
76	35	66.0	85	2	Q4YD72_PLABE	Q4YD72 plasmodium
77	35	66.0	133	2	Q4MMJ5_BACCE	Q4MMJ5 bacillus ce
78	35	66.0	147	2	Q8YMC1_ANASP	Q8YMC1 anabaena sp
79	35	66.0	148	2	Q6HK12_BACHK	Q6HK12 bacillus th
80	35	66.0	148	2	Q8IEM1_BACCR	Q8IEM1 bacillus ce
81	35	66.0	148	2	Q739V7_BACCI	Q739V7 bacillus ce
82	35	66.0	148	2	Q81RT9_BACAN	Q81RT9 bacillus an
83	35	66.0	148	2	Q63CK7_BACCC	Q63CK7 bacillus ce
84	35	66.0	185	2	Q694F4_LISMO	Q694F4 listeria mo
85	35	66.0	187	2	Q7KMU7_DICDI	Q7KMU7 dictyosteli
86	35	66.0	229	2	Q4Y010_PLACH	Q4Y010 plasmodium
87	35	66.0	235	2	Q559J3_DICDI	Q559J3 dictyosteli
88	35	66.0	252	2	Q7LV9_CLOAB	Q7LV9 clostridium
89	35	66.0	258	2	Q4SP53_TETNG	Q4SP53 tetraodon n
90	35	66.0	343	2	Q5VR28_ORYSA	Q5VR28 oryza sativ
91	35	66.0	367	2	Q8I371_PLAF7	Q8I371 plasmodium
92	35	66.0	401	2	Q4MWA7_BACCE	Q4MWA7 bacillus ce
93	35	66.0	401	2	Q81UF1_BACAN	Q81UF1 bacillus an
94	35	66.0	402	2	Q812N2_BACAN	Q812N2 bacillus an
95	35	66.0	424	2	Q4MGP21_BACCE	Q4MGP21 bacillus ce
96	35	66.0	424	2	Q6HF27_BACHK	Q6HF27 bacillus th
97	35	66.0	424	2	Q732T8_BACCI	Q732T8 bacillus ce
98	35	66.0	424	2	Q81A08_BACCR	Q81A08 bacillus an
99	35	66.0	424	2	Q81WP6_BACAN	Q81WP6 bacillus an
100	35	66.0	424	2	Q636N8_BACCC	Q636N8 bacillus ce
101	35	66.0	425	2	Q7X275_9RHIZ	Q7X275 bartonella
102	35	66.0	426	2	Q6FPYK4_BAROU	Q6FPYK4 bartonella
103	35	66.0	433	2	Q7RTF2_PLABO	Q7RTF2 plasmodium
104	35	66.0	455	2	Q4YXU4_PLABE	Q4YXU4 plasmodium

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:19:39 ; Search time 16.6667 Seconds
(without alignments)
57.730 Million cell updates/sec

Title: US-10-091-135-13
Perfect score: 53
Sequence: 1 FKNEELYQTK 10

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

PIR 80:*
1: Pirl.*
2: Pirl.*
3: Pirl.*
4: Pirl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	49	92.5	204	2 B37329	antigen 5 - easter
2	49	92.5	204	2 A44583	venom allergen ant
3	46	86.8	204	2 B44583	venom allergen ant
4	46	86.8	204	2 C44583	venom allergen ant
5	44	83.0	346	2 G72094	ct244 hypothetical
6	44	83.0	346	2 G86528	CT244 hypothetical
7	44	83.0	346	2 B81574	conserved hypothet
8	37	69.8	206	2 E44583	venom allergen ant
9	37	69.8	416	2 C71620	protein with Egl-1
10	37	69.8	4859	2 S74173	ryanodine receptor
11	37	69.8	4872	2 S27272	ryanodine receptor
12	36	67.9	244	2 A01834	isopentenyl transf
13	36	67.9	387	2 E82881	hypothetical prote
14	35	66.0	147	2 AE2432	hypothetical prote
15	35	66.0	252	2 F96954	protein, containin
16	35	66.0	485	2 T24115	hypothetical prote
17	35	66.0	572	2 AC1200	phosphotransferase
18	35	66.0	572	2 A11557	DNA topoisomerase
19	35	66.0	599	2 D70104	hypothetical prote
20	35	66.0	599	2 C90561	ryanodine receptor
21	35	66.0	4869	2 S66572	T-cell surface gly
22	34	64.2	173	1 RWSMD2	T-cell surface gly
23	34	64.2	173	2 S10975	response regulator
24	34	64.2	370	2 F84151	probable hth trans
25	34	64.2	392	2 H71520	heat shock gene re
26	34	64.2	392	2 F81676	HTH transcription
27	34	64.2	398	2 A86553	hth transcription
28	34	64.2	398	2 G72070	heat shock gene re
29	34	64.2	407	2 B81598	

30	64.2	620	2	S38994	origin recognition
31	64.2	630	2	H82823	conserved hypothet
32	64.2	3394	2	T18501	hypothetical prote
33	62.3	254	2	S55136	probable cytoskele
34	62.3	279	2	S52582	prephenate dehydra
35	62.3	297	2	S66102	protein secretion
36	62.3	453	2	B49022	tryptophanase (EC
37	62.3	454	2	B84699	hypothetical prote
38	62.3	478	1	T05423	probable glucosylt
39	62.3	505	1	S13744	glucose-6-phosphat
40	62.3	512	2	T14638	cytochrome P450 CY
41	62.3	596	2	G82874	conserved hypothet
42	62.3	636	2	I61718	neu differentiation
43	62.3	637	2	C43273	heregulin precursor
44	62.3	701	2	S35313	TIP1 protein - yea
45	62.3	779	2	T20654	hypothetical prote
46	62.3	1082	2	T41988	hypothetical prote
47	62.3	1186	2	C64588	cag pathogenicity
48	62.3	1291	2	S02021	micropia polyprote
49	62.3	1302	1	RRXRBT	RNA-directed RNA p
50	62.3	2314	1	A46151	protein-tyrosine-p
51	62.3	2925	1	T00133	RNA-directed RNA p
52	60.4	76	2	T42309	hypothetical prote
53	60.4	78	2	H70020	hypothetical prote
54	60.4	82	1	CCAV5	cytochrome c551 -
55	60.4	107	2	F86869	hypothetical prote
56	60.4	149	2	D69666	nucleoside-diphosp
57	60.4	220	2	S45927	probable finger pr
58	60.4	274	2	T12791	hypothetical prote
59	60.4	287	2	E95313	cytochrome-c oxida
60	60.4	297	2	F64206	lipopolysaccharide
61	60.4	298	2	G64465	modification mech
62	60.4	326	2	AB1431	Arac-type regulato
63	60.4	326	2	AH1804	Arac-type regulato
64	60.4	332	2	T24312	hypothetical prote
65	60.4	334	2	F89008	protein W08A12.4 [
66	60.4	371	2	T44297	response regulator
67	60.4	393	2	AD2376	transcription regu
68	60.4	448	2	C97757	hypothetical prote
69	60.4	476	2	I37136	adenylate cyclase
70	60.4	478	2	JQ2034	RNA-directed RNA p
71	60.4	489	2	H64224	hypothetical prote
72	60.4	492	2	T21797	hypothetical prote
73	60.4	503	2	C84595	similar to pEARL1
74	60.4	504	2	A86190	hypothetical prote
75	60.4	540	2	D86432	tRNA-pseudouridine
76	60.4	544	2	S65231	hypothetical prote
77	60.4	548	2	T18761	hypothetical prote
78	60.4	604	2	S15794	lin-9 protein - Ca
79	60.4	608	2	T18437	hypothetical prote
80	60.4	610	2	A88542	hypothetical prote
81	60.4	634	2	G90779	hypothetical prote
82	60.4	635	2	S75668	DNA primase (EC 2.
83	60.4	645	2	A85641	hypothetical prote
84	60.4	689	2	F81286	probable polysacch
85	60.4	723	2	H85092	hypothetical prote
86	60.4	751	2	T21967	hypothetical prote
87	60.4	758	2	C96749	hypothetical prote
88	60.4	844	2	S47274	membrane alanyl am
89	60.4	844	2	JC4054	membrane alanyl am
90	60.4	848	2	G90128	elongation factor
91	60.4	971	2	C82880	conserved hypothet
92	60.4	1047	2	T34946	probable isoleucyl
93	60.4	1090	2	A41541	adenylate cyclase
94	60.4	1092	2	T18354	adhesin - Mycoplas
95	60.4	1099	2	T18357	mup1 protein - Myc
96	60.4	1102	2	S65235	probable membrane
97	60.4	1108	2	T18353	reverse gyrase - A
98	60.4	1171	2	G70399	gene u-shaped prot
99	60.4	1191	2	T13850	exodeoxyribonuclea
100	60.4	1211	2	D64116	valine-tRNA ligase
101	60.4	1296	2	S55511	hypothetical prote
102	58.5	105	2	H97704	

98	33	62.3	19	2	AAR56635	Aar56635 Tyrosine	171	33	62.3	5	ABJ00060	Abj00060 Human neu
99	33	62.3	63	3	AAB36703	Aab36703 EGF-like	172	33	62.3	2	AAR68576	Aar68576 Rat NDF e
100	33	62.3	63	3	AAB36707	Aab36707 EGF-like	173	33	62.3	2	AAR68573	Aar68573 Rat NDF e
101	33	62.3	119	4	AAG67932	Aag67932 Human NRG	174	33	62.3	2	AAR29573	Aar29573 Human her
102	33	62.3	119	4	AAG67970	Aag67970 Human NRG	175	33	62.3	2	AAV06636	Aav06636 Herugelin
103	33	62.3	119	5	ABJ00042	Abj00042 Human neu	176	33	62.3	3	AAV71173	Aav71173 Human Her
104	33	62.3	119	5	ABJ00080	Abj00080 Human neu	177	33	62.3	3	AAV71173	Aav71173 Human Her
105	33	62.3	119	7	ADW70324	Adw70324 Human neu	178	33	62.3	3	AAU09888	Aau09888 Human NRG
106	33	62.3	119	8	ADH77519	Adh77519 Human neu	179	33	62.3	3	AAU09888	Aau09888 Human NRG
107	33	62.3	129	4	AAG67931	Aag67931 Human NRG	180	33	62.3	3	AAU09888	Aau09888 Human NRG
108	33	62.3	129	4	AAG67969	Aag67969 Human NRG	181	33	62.3	3	AAU09888	Aau09888 Human NRG
109	33	62.3	129	5	ABJ00041	Abj00041 Human neu	182	33	62.3	3	AAU09888	Aau09888 Human NRG
110	33	62.3	129	5	ABJ00079	Abj00079 Human neu	183	33	62.3	3	AAU09888	Aau09888 Human NRG
111	33	62.3	129	7	ADW70323	Adw70323 Human neu	184	33	62.3	3	AAU09888	Aau09888 Human NRG
112	33	62.3	129	8	ADH77518	Adh77518 Human neu	185	33	62.3	3	AAU09888	Aau09888 Human NRG
113	33	62.3	167	9	ADY28391	Ady28391 Novel Erb	186	33	62.3	3	AAU09888	Aau09888 Human NRG
114	33	62.3	192	4	AAG67900	Aag67900 Human neu	187	33	62.3	3	AAU09888	Aau09888 Human NRG
115	33	62.3	192	4	AAG67938	Aag67938 Human neu	188	33	62.3	3	AAU09888	Aau09888 Human NRG
116	33	62.3	192	5	ABJ00010	Abj00010 Human neu	189	33	62.3	3	AAU09888	Aau09888 Human NRG
117	33	62.3	192	5	ABJ00048	Abj00048 Human neu	190	33	62.3	3	AAU09888	Aau09888 Human NRG
118	33	62.3	192	7	ADW70292	Adw70292 Human neu	191	33	62.3	3	AAU09888	Aau09888 Human NRG
119	33	62.3	192	8	ADH77487	Adh77487 Human neu	192	33	62.3	3	AAU09888	Aau09888 Human NRG
120	33	62.3	253	3	AAB24132	Aab24132 Plasmodiu	193	33	62.3	3	AAU09888	Aau09888 Human NRG
121	33	62.3	276	2	AAR68586	Aar68586 Human pro	194	33	62.3	3	AAU09888	Aau09888 Human NRG
122	33	62.3	282	4	ABB66530	Abb66530 Drosophil	195	33	62.3	3	AAU09888	Aau09888 Human NRG
123	33	62.3	284	5	ABU51953	Abu51953 Helicobac	196	33	62.3	3	AAU09888	Aau09888 Human NRG
124	33	62.3	298	2	AAR68575	Aar68575 Rat NDF e	197	33	62.3	3	AAU09888	Aau09888 Human NRG
125	33	62.3	300	2	AAW11503	Aaw11503 Humanised	198	33	62.3	3	AAU09888	Aau09888 Human NRG
126	33	62.3	300	2	AAW73218	Aaw73218 H22-HRG f	199	33	62.3	3	AAU09888	Aau09888 Human NRG
127	33	62.3	300	4	AAB61954	Aab61954 Amino aci	200	33	62.3	3	AAU09888	Aau09888 Human NRG
128	33	62.3	300	4	AAB85449	Aab85449 H22-HRG f	201	33	62.3	3	AAU09888	Aau09888 Human NRG
129	33	62.3	316	8	ADX66573	Adx66573 Plant ful	202	33	62.3	3	AAU09888	Aau09888 Human NRG
130	33	62.3	323	3	AAG21801	Aag21801 Arabidops	203	33	62.3	3	AAU09888	Aau09888 Human NRG
131	33	62.3	323	3	AAG40014	Aag40014 Arabidops	204	33	62.3	3	AAU09888	Aau09888 Human NRG
132	33	62.3	326	6	ABU44164	Abu44164 Protein e	205	32	60.4	3	AAU09888	Aau09888 Human NRG
133	33	62.3	335	3	AAG21800	Aag21800 Arabidops	206	32	60.4	3	AAU09888	Aau09888 Human NRG
134	33	62.3	335	3	AAG40013	Aag40013 Arabidops	207	32	60.4	3	AAU09888	Aau09888 Human NRG
135	33	62.3	348	4	ABB50156	Abb50156 Human tra	208	32	60.4	3	AAU09888	Aau09888 Human NRG
136	33	62.3	348	5	ABW48914	Aab48914 Human tra	209	32	60.4	3	AAU09888	Aau09888 Human NRG
137	33	62.3	348	5	ABP64715	Abp64715 Human pro	210	32	60.4	3	AAU09888	Aau09888 Human NRG
138	33	62.3	356	5	ABU51625	Abu51625 Helicobac	211	32	60.4	3	AAU09888	Aau09888 Human NRG
139	33	62.3	374	3	AAG21799	Aag21799 Arabidops	212	32	60.4	3	AAU09888	Aau09888 Human NRG
140	33	62.3	374	3	AAG40012	Aag40012 Arabidops	213	32	60.4	3	AAU09888	Aau09888 Human NRG
141	33	62.3	377	8	ADP98902	Adp98902 C. albica	214	32	60.4	3	AAU09888	Aau09888 Human NRG
142	33	62.3	378	4	ABBE6800	Abbe6800 Drosophil	215	32	60.4	3	AAU09888	Aau09888 Human NRG
143	33	62.3	379	5	ABBE6800	Abbe6800 Drosophil	216	32	60.4	3	AAU09888	Aau09888 Human NRG
144	33	62.3	389	5	ABU50882	Abu50882 Helicobac	217	32	60.4	3	AAU09888	Aau09888 Human NRG
145	33	62.3	420	2	AAR29575	Aar29575 Human her	218	32	60.4	3	AAU09888	Aau09888 Human NRG
146	33	62.3	420	2	AAY06638	Aay06638 Herugelin	219	32	60.4	3	AAU09888	Aau09888 Human NRG
147	33	62.3	420	2	AAV71175	Aav71175 Human her	220	32	60.4	3	AAU09888	Aau09888 Human NRG
148	33	62.3	420	4	AAU09890	Aau09890 Human her	221	32	60.4	3	AAU09888	Aau09888 Human NRG
149	33	62.3	420	5	ABU51367	Abu51367 Helicobac	222	32	60.4	3	AAU09888	Aau09888 Human NRG
150	33	62.3	422	5	ABU51614	Abu51614 Helicobac	223	32	60.4	3	AAU09888	Aau09888 Human NRG
151	33	62.3	438	7	ABW87032	Abw87032 Rice abio	224	32	60.4	3	AAU09888	Aau09888 Human NRG
152	33	62.3	454	3	ABB08439	Abb08439 Recombina	225	32	60.4	3	AAU09888	Aau09888 Human NRG
153	33	62.3	460	3	AAG40011	Aag40011 Arabidops	226	32	60.4	3	AAU09888	Aau09888 Human NRG
154	33	62.3	465	3	AAG40010	Aag40010 Arabidops	227	32	60.4	3	AAU09888	Aau09888 Human NRG
155	33	62.3	465	8	ADH43026	Adh43026 IPT-like	228	32	60.4	3	AAU09888	Aau09888 Human NRG
156	33	62.3	478	5	ABB93231	Abb93231 Herbicida	229	32	60.4	3	AAU09888	Aau09888 Human NRG
157	33	62.3	480	7	ABW90074	Abw90074 Rice abio	230	32	60.4	3	AAU09888	Aau09888 Human NRG
158	33	62.3	481	3	AAG40009	Aag40009 Arabidops	231	32	60.4	3	AAU09888	Aau09888 Human NRG
159	33	62.3	481	4	AAE07509	Aae07509 Arabidops	232	32	60.4	3	AAU09888	Aau09888 Human NRG
160	33	62.3	481	8	ADN72645	Adn72645 Thale cre	233	32	60.4	3	AAU09888	Aau09888 Human NRG
161	33	62.3	505	8	ADN19239	Adn19239 Bacterial	234	32	60.4	3	AAU09888	Aau09888 Human NRG
162	33	62.3	512	6	ADA48020	Ada48020 Rice prot	235	32	60.4	3	AAU09888	Aau09888 Human NRG
163	33	62.3	512	6	ADA480748	Ada480748 Rice prot	236	32	60.4	3	AAU09888	Aau09888 Human NRG
164	33	62.3	515	8	ADY13102	Ady13102 Plant ful	237	32	60.4	3	AAU09888	Aau09888 Human NRG
165	33	62.3	536	8	ADT56220	Adt56220 Plant pol	238	32	60.4	3	AAU09888	Aau09888 Human NRG
166	33	62.3	596	6	ABU48987	Abu48987 Protein e	239	32	60.4	3	AAU09888	Aau09888 Human NRG
167	33	62.3	604	8	ADN26327	Adn26327 Bacterial	240	32	60.4	3	AAU09888	Aau09888 Human NRG
168	33	62.3	623	7	ADC95099	Adc95099 E. faeciu	241	32	60.4	3	AAU09888	Aau09888 Human NRG
169	33	62.3	629	8	ADH77499	Adh77499 Human neu	242	32	60.4	3	AAU09888	Aau09888 Human NRG
170	33	62.3	631	5	ABJ00022	Abj00022 Human neu	243	32	60.4	3	AAU09888	Aau09888 Human NRG

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:13:51 ; Search time 87.9167 Seconds
(without alignment)
49.977 Million cell updates/sec

Title: US-10-091-135-13

Perfect score: 53

Sequence: 1 FKNEELYQTK 10

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A Geneseq_21.*

1: Geneseqp1980s.*

2: Geneseqp1980s.*

3: Geneseqp2000s.*

4: Geneseqp2001s.*

5: Geneseqp2002s.*

6: Geneseqp2003as.*

7: Geneseqp2003bs.*

8: Geneseqp2004s.*

9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	53	100.0	10	5	Aae28819
2	53	100.0	49	5	Aae28814
3	53	100.0	204	2	Aay45217
4	53	100.0	204	5	Abg66977
5	53	100.0	204	5	Abg66983
6	53	100.0	204	5	Abg67052
7	53	100.0	204	5	Abg67104
8	53	100.0	204	5	Abg67103
9	53	100.0	204	5	Aae28820
10	53	100.0	209	4	Abm00031
11	49	92.5	204	2	Aaw35687
12	47	88.7	204	2	Aaw35688
13	47	88.7	227	2	Aay25644
14	47	88.7	227	4	Aae13071
15	47	88.7	227	7	Adc34893
16	44	83.0	354	2	Aay34899
17	39	73.6	1235	8	Adp98882
18	38	71.7	604	3	Aab16502
19	37	69.8	206	2	Aay25648
20	37	69.8	206	7	Adc34897
21	37	69.8	416	3	Aab18185
22	37	69.8	674	4	Abp62357
23	37	69.8	1425	4	Abg23344
24	37	69.8	4771	4	Aau02939

25	37	69.8	4866	2	AAW77410	Human tya
26	37	69.8	4899	4	ABG12314	Novel hum
27	37	69.8	4899	7	ADF60293	Human con
28	37	69.8	4934	4	ABG23346	Novel hum
29	36	67.9	71	4	AAG75080	Human col
30	36	67.9	86	5	ABP42496	Human ova
31	36	67.9	135	3	AAB38300	Human sec
32	36	67.9	135	3	AAB38299	Human sec
33	36	67.9	135	3	AAB38305	Human sec
34	36	67.9	135	3	AAB38306	Human sec
35	36	67.9	136	8	ADR43249	IPT-like
36	36	67.9	136	8	ADS29720	Bacterial
37	36	67.9	152	4	AAO2594	Human pol
38	36	67.9	244	8	ADR43143	IPT-like
39	36	67.9	310	6	ABU70525	Human adi
40	36	67.9	1097	6	Aao30432	Human kar
41	36	67.9	1097	6	ADJ57062	Human kar
42	36	67.9	1097	8	ADO19838	Human PRO
43	36	67.9	1097	8	ADQ18847	Human sof
44	36	67.9	1097	8	ADP54967	Human PRO
45	36	67.9	1105	4	AAW40174	Human pol
46	36	67.9	1105	4	ABG05389	Novel hum
47	36	67.9	1105	6	AAO30433	Human RAN
48	36	67.9	1105	8	ADS8209	Human PRO
49	36	67.9	1115	8	ADL13164	Human ste
50	36	67.9	1126	4	ABG30229	Novel hum
51	36	67.9	3692	6	ABU43311	Protein e
52	36	67.9	3692	8	ADS20647	S. epider
53	36	67.9	3696	5	ABP40235	Staphyloc
54	36	67.9	3696	8	ADS06647	Staphyloc
55	35	66.0	152	6	ADB09334	Alloioococ
56	35	66.0	427	8	ADT92052	Sugar bee
57	35	66.0	485	8	ADT23927	Bacterial
58	35	66.0	572	5	ABB49227	Listeria
59	35	66.0	572	6	ABU32704	Protein e
60	35	66.0	798	3	AAB25551	Eucalyptu
61	35	66.0	1240	4	ABB61596	Drosophil
62	35	66.0	4544	2	ADP25443	Plasmodiu
63	34	64.2	20	2	AAR79995	ARH1 pept
64	34	64.2	26	3	AAV52320	Multisubu
65	34	64.2	26	6	ABU08907	Mouse imm
66	34	64.2	26	7	ADH74786	Mouse imm
67	34	64.2	57	9	ABM96055	M. xanthu
68	34	64.2	109	8	ADT87653	Plant hom
69	34	64.2	215	4	AAG81867	S. epider
70	34	64.2	224	5	ABP40450	Staphyloc
71	34	64.2	224	8	ADS05989	Staphyloc
72	34	64.2	240	8	ADX73822	Plant ful
73	34	64.2	287	6	ADB07250	Alloioococ
74	34	64.2	302	8	ADN74187	Thale cre
75	34	64.2	304	2	AAV35123	Chlamydia
76	34	64.2	311	6	ADB07252	Alloioococ
77	34	64.2	314	6	ADB07254	Alloioococ
78	34	64.2	387	6	ABU24476	Protein e
79	34	64.2	392	2	AAV36778	Protein i
80	34	64.2	422	8	ADX96929	Plant ful
81	34	64.2	485	4	AAV95017	Human pro
82	34	64.2	485	7	ADJ86637	Human hea
83	34	64.2	517	8	ADX92973	Plant ful
84	34	64.2	603	8	ADY04542	Plant ful
85	34	64.2	620	2	AAR77275	ORC2 subu
86	34	64.2	620	5	AAU82999	S. cerevi
87	34	64.2	620	6	ABR53643	Protein s
88	34	64.2	620	7	ADN64130	Disease t
89	34	64.2	620	8	ADN18789	Bacterial
90	34	64.2	645	8	ADX93364	Plant ful
91	34	64.2	749	8	ADR10498	Mouse pro
92	34	64.2	820	4	AAU35178	Enterococ
93	34	64.2	824	7	ADH87023	Enterococ
94	34	64.2	824	7	ADH87023	Enterococ
95	33	62.3	19	2	AAR56641	Tyrosine
96	33	62.3	19	2	AAR56636	Tyrosine
97	33	62.3	19	2	AAR56642	Tyrosine

99	29	69.0	915	7	US-11-205-935-16	Sequence 16, Appl	172	28	65.7	852	6	US-10-725-475-7	Sequence 7, Appl
100	29	69.0	915	7	US-11-205-935-22	Sequence 22, Appl	173	28	66.7	852	7	US-11-050-804-6	Sequence 6, Appl
101	29	69.0	917	7	US-11-144-987-18	Sequence 18, Appl	174	28	66.7	875	7	US-11-087-039-7790	Sequence 7790, Ap
102	29	69.0	917	7	US-11-144-987-20	Sequence 20, Appl	175	28	66.7	875	7	US-11-188-298-18220	Sequence 18220, A
103	29	69.0	917	7	US-11-144-987-24	Sequence 24, Appl	176	28	66.7	885	7	US-11-072-512-2946	Sequence 2946, Ap
104	29	69.0	917	7	US-11-144-987-26	Sequence 26, Appl	177	28	66.7	885	6	US-10-517-939-258	Sequence 258, App
105	29	69.0	917	7	US-11-205-935-18	Sequence 18, Appl	178	28	66.7	1075	6	US-10-745-586-197	Sequence 197, App
106	29	69.0	917	7	US-11-205-935-20	Sequence 20, Appl	179	28	66.7	1483	7	US-11-188-298-10839	Sequence 10839, A
107	29	69.0	917	7	US-11-205-935-24	Sequence 24, Appl	180	28	66.7	1518	7	US-11-087-039-1886	Sequence 1886, Ap
108	29	69.0	917	7	US-11-205-935-26	Sequence 26, Appl	181	28	66.7	1827	7	US-11-057-058-62	Sequence 62, Appl
109	29	69.0	1306	6	US-10-995-561-905	Sequence 905, App	182	28	66.7	2051	6	US-10-330-773-307	Sequence 307, App
110	29	69.0	1356	6	US-10-995-561-904	Sequence 904, App	183	28	66.7	2304	6	US-10-330-773-310	Sequence 310, App
111	29	69.0	1356	6	US-10-995-561-906	Sequence 906, App	184	27	64.3	55	7	US-11-183-567A-8	Sequence 8, Appl
112	29	69.0	1410	6	US-10-878-556A-136	Sequence 136, App	185	27	64.3	85	7	US-11-096-568A-7502	Sequence 7502, Ap
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133	28	66.7	276	7	US-11-087-099-9294	Sequence 9294, Ap	206	27	64.3	291	7	US-11-087-099-6931	Sequence 6931, Ap
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149	28	66.7	419	7	US-11-188-298-16741	Sequence 16741, A	222	27	64.3	348	7	US-11-096-568A-23132	Sequence 23132, A
150	28	66.7	420	7	US-11-188-298-741	Sequence 741, App	223	27	64.3	348	7	US-11-188-298-15790	Sequence 15790, A
151	28	66.7	435	7	US-11-188-298-8860	Sequence 8860, Ap	224	27	64.3	352	7	US-11-096-568A-32479	Sequence 32479, A
152	28	66.7	466	6	US-10-979-095-1	Sequence 1, Appl	225	27	64.3	355	7	US-11-188-298-709	Sequence 709, App
153	28	66.7	472	7	US-11-188-298-3743	Sequence 3743, Ap	226	27	64.3	357	7	US-11-096-568A-29973	Sequence 29973, A
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162	28	66.7	574	6	US-10-195-883-234	Sequence 234, App	235	27	64.3	398	7	US-11-096-568A-6867	Sequence 6867, Ap
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46.352 Million cell updates/sec

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Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	34	81.0	457	6	US-10-877-346-49
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6	33	78.6	53	6	US-10-895-064-2440
7	33	78.6	53	7	US-11-129-741-2440
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9	33	78.6	855	7	US-11-087-099-12274
10	33	78.6	1166	7	US-11-188-298-11021
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13	32	76.2	389	7	US-11-188-298-21334
14	32	76.2	405	7	US-11-079-463-6011
15	32	76.2	508	7	US-11-087-099-5716
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19	31	73.8	475	6	US-10-877-346-48
20	31	73.8	477	6	US-10-877-346-47
21	31	73.8	480	6	US-10-877-346-15
22	31	73.8	486	6	US-10-877-346-50
23	31	73.8	490	7	US-11-072-512-3841
24	31	73.8	619	7	US-11-096-568A-20917
25	31	73.8	625	7	US-11-096-568A-20916

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29	31	73.8	4346	6	US-10-995-561-671	Sequence 671, App
30	31	73.8	4347	6	US-10-995-561-670	Sequence 670, App
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46	29	69.0	231	7	US-11-188-298-14354	Sequence 14354, A
47	29	69.0	242	7	US-11-188-298-3157	Sequence 3157, Ap
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57	29	69.0	309	7	US-11-087-099-4759	Sequence 4759, Ap
58	29	69.0	310	7	US-11-087-099-6235	Sequence 6235, Ap
59	29	69.0	310	7	US-11-087-099-12084	Sequence 12084, A
60	29	69.0	311	7	US-11-096-568A-7222	Sequence 7222, Ap
61	29	69.0	327	7	US-11-087-099-5493	Sequence 5493, Ap
62	29	69.0	330	7	US-11-074-176-174	Sequence 174, App
63	29	69.0	330	7	US-11-087-099-2823	Sequence 2823, Ap
64	29	69.0	332	7	US-11-087-099-3470	Sequence 3470, Ap
65	29	69.0	332	7	US-11-096-568A-11527	Sequence 11527, A
66	29	69.0	350	7	US-11-188-298-335	Sequence 335, App
67	29	69.0	363	7	US-11-188-298-6356	Sequence 6356, Ap
68	29	69.0	381	6	US-10-501-035-223	Sequence 223, App
69	29	69.0	389	7	US-11-188-298-572	Sequence 572, App
70	29	69.0	389	7	US-11-188-298-1874	Sequence 1874, Ap
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78	29	69.0	404	7	US-11-188-298-19850	Sequence 19850, A
79	29	69.0	405	7	US-11-087-099-11914	Sequence 11914, A
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81	29	69.0	429	7	US-11-096-568A-7221	Sequence 7221, Ap
82	29	69.0	435	7	US-11-079-463-7935	Sequence 7935, Ap
83	29	69.0	456	7	US-11-188-298-21690	Sequence 21690, A
84	29	69.0	457	6	US-10-467-657-6640	Sequence 6640, Ap
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86	29	69.0	481	7	US-11-096-568A-7220	Sequence 7220, Ap
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88	29	69.0	519	7	US-11-096-568A-24188	Sequence 24188, A
89	29	69.0	542	7	US-11-013-592-40	Sequence 40, Appl
90	29	69.0	566	7	US-11-096-568A-24187	Sequence 24187, A
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92	29	69.0	764	7	US-11-104-111-28	Sequence 28, Appl
93	29	69.0	767	7	US-11-075-047A-4	Sequence 4, Appl1
94	29	69.0	767	7	US-11-043-693-2	Sequence 2, Appl1
95	29	69.0	816	7	US-11-090-439-48	Sequence 48, Appl
96	29	69.0	915	7	US-11-144-987-16	Sequence 16, Appl
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104	32	76.2	155	4	US-10-437-963-163298	Sequence 163298, Ap	177	31	73.8	327	5	US-10-764-260-9	Sequence 9, Appl
105	32	76.2	190	4	US-10-437-963-193374	Sequence 193374, Ap	178	31	73.8	330	5	US-10-472-928-4104	Sequence 4104, Ap
106	32	76.2	212	4	US-10-768-093-7	Sequence 7, Appl	179	31	73.8	332	4	US-10-474-776-722	Sequence 722, App
107	32	76.2	217	4	US-10-424-599-284928	Sequence 284928, Ap	180	31	73.8	335	4	US-10-017-161-694	Sequence 694, App
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109	32	76.2	296	4	US-10-425-115-266787	Sequence 266787, Ap	182	31	73.8	355	4	US-10-292-798-632	Sequence 632, App
110	32	76.2	326	4	US-10-369-493-9804	Sequence 9804, Ap	183	31	73.8	357	4	US-10-424-599-252964	Sequence 252964, Ap
111	32	76.2	383	3	US-09-339-853A-22	Sequence 22, Appl	184	31	73.8	388	4	US-10-425-115-286991	Sequence 286991, Ap
112	32	76.2	425	4	US-10-437-963-176705	Sequence 176705, Ap	185	31	73.8	394	3	US-09-817-513A-4	Sequence 4, Appl
113	32	76.2	432	4	US-10-289-762-321	Sequence 321, App	186	31	73.8	416	4	US-10-425-114-64456	Sequence 64456, A
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117	32	76.2	505	4	US-10-437-963-115721	Sequence 115721, Ap	190	31	73.8	475	3	US-09-964-956-48	Sequence 48, Appl
118	32	76.2	511	3	US-09-893-519A-23	Sequence 23, Appl	191	31	73.8	475	3	US-10-299-642-24	Sequence 24, Appl
119	32	76.2	511	4	US-10-369-493-1888	Sequence 1888, Ap	192	31	73.8	477	3	US-09-826-503-493	Sequence 493, App
120	32	76.2	591	4	US-10-424-599-285635	Sequence 285635, Ap	193	31	73.8	477	3	US-09-964-956-47	Sequence 47, Appl
121	32	76.2	614	4	US-10-369-493-10317	Sequence 10317, A	194	31	73.8	477	4	US-10-277-078-2	Sequence 2, Appl
122	32	76.2	661	4	US-10-160-865-14	Sequence 14, Appl	195	31	73.8	477	4	US-10-277-078-3	Sequence 3, Appl
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134	32	76.2	3208	4	US-10-210-130-36	Sequence 36, Appl	207	31	73.8	540	4	US-10-112-944-876	Sequence 876, App
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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21	35	83.3	204	4	US-10-719-553-39
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45	34	81.0	446	4	US-10-299-642-22	Sequence 22, Appl
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139	29	69.0	290	2	US-09-857-896A-2	Sequence 2, Appl	212	29	59.0	917	2	US-10-282-162-50	Sequence 50, Appl
140	29	69.0	298	2	US-09-328-352-5270	Sequence 5270, A	213	29	59.0	917	2	US-10-282-162-54	Sequence 54, Appl
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153	29	69.0	388	2	US-09-191-608-23	Sequence 23, Appl	226	29	59.0	1463	1	US-08-220-603A-11	Sequence 11, Appl
154	29	69.0	388	2	US-08-091-519-2	Sequence 2, Appl	227	29	59.0	2304	2	US-09-324-867-4	Sequence 4, Appl
155	29	69.0	398	1	US-08-442-043A-2	Sequence 2, Appl	228	29	59.0	2319	1	US-08-212-133A-8	Sequence 8, Appl
156	29	69.0	398	2	US-09-173-151A-26	Sequence 26, Appl	229	29	59.0	2319	1	US-08-474-503-6	Sequence 6, Appl
157	29	69.0	398	2	US-09-461-908-2	Sequence 2, Appl	230	29	59.0	2319	1	US-08-670-707A-6	Sequence 6, Appl
158	29	69.0	398	2	US-08-441-893A-2	Sequence 2, Appl	231	29	59.0	2319	2	US-09-037-601-6	Sequence 6, Appl
159	29	69.0	398	2	US-09-579-845-4	Sequence 4, Appl	232	29	59.0	2319	2	US-09-315-179-6	Sequence 6, Appl
160	29	69.0	398	2	US-08-406-824A-8	Sequence 8, Appl	233	29	59.0	2319	4	PCT-US94-13200-6	Sequence 28, Appl
161	29	69.0	398	2	US-09-921-667-8	Sequence 8, Appl	234	29	59.0	2596	2	US-09-548-473B-6	Sequence 28, Appl
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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5	35	83.3	204	2	US-09-130-287-2
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13	34	81.0	446	1	US-08-333-977-22
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17	34	81.0	446	2	US-10-277-078-4
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34	31	73.8	100	2	US-09-270-767-55787	Sequence 55787, A
35	31	73.8	151	2	US-09-270-767-45274	Sequence 45274, A
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70	30	71.4	123	2	US-10-004-860-780	Sequence 780, App
71	30	71.4	141	2	US-09-328-352-5789	Sequence 5789, Ap
72	30	71.4	143	2	US-09-270-767-37046	Sequence 37046, A
73	30	71.4	143	2	US-09-270-767-52263	Sequence 52263, A
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113	33	78.6	424	2	Q4NDL4 9NICC	Q4ndl4 arthrobacte	186	32	76.2	344	2	Q4JOB6 AZOVI	Q4job6 azotobacter
114	33	78.6	430	2	Q60UD3 CAEBR	Q60ud3 caenorhabdi	187	32	76.2	345	2	Q4UEL4 THEAN	Q4uel4 theileria a
115	33	78.6	433	2	Q6WAE4 PARUM	Q6wae4 parachlamyd	188	32	76.2	359	1	REBG SALTU	P26397 salmonella
116	33	78.6	444	2	Q7LZ73 CHICK	Q7l773 gallus gall	189	32	76.2	359	2	Q8Z515 SALTU	Q8z515 salmonella
117	33	78.6	462	2	Q54VQ5 DICI	Q54vq5 dictyosteli	190	32	76.2	378	2	Q5PE01 SALPA	Q5pe01 salinobacil
118	33	78.6	463	2	Q54IJ3 DICI	Q54ij3 dictyosteli	191	32	76.2	378	2	Q5OH17 ACTPL	Q5oh17 actinobacil
119	33	78.6	466	1	DCEA ECO57	P58228 escherichia	192	32	76.2	379	2	Q4IQ70 GIBZE	Q4iq70 gibberella
120	33	78.6	466	1	DCEA ECO16	P69909 escherichia	193	32	76.2	380	2	Q5OH23 ACTPL	Q5oh23 actinobacil
121	33	78.6	466	1	DCEA ECO1	P69908 escherichia	194	32	76.2	381	2	Q6UYC5 ACTPL	Q6uyc5 actinobacil
122	33	78.6	466	1	DCEA SHIFL	Q83pr1 shigella fl	195	32	76.2	382	2	Q5OH23 ACTPL	Q5oh23 actinobacil
123	33	78.6	466	1	DCEB ECO57	P69911 escherichia	196	32	76.2	383	2	Q6V013 ACTPL	Q6v013 actinobacil
124	33	78.6	466	1	DCEB ECO16	Q8fig5 escherichia	197	32	76.2	385	2	Q4IIE1 GIBZE	Q4iie1 gibberella
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126	33	78.6	466	1	DCEB SHIFL	P69912 shigella fl	199	32	76.2	389	2	P7A2B1 ANOSP	P7a2b1 anabaena ep
127	33	78.6	474	2	Q6ARB0 DESFS	Q6arb0 desulfotale	200	32	76.2	389	2	Q8VRP4 ANASP	Q8vrp4 anabaena ep
128	33	78.6	513	2	Q6FSG1 CANGA	Q6fsg1 candida gla	201	32	76.2	391	2	Q9R6X5 ANASP	Q9r6x5 anabaena ep
129	33	78.6	539	2	Q7PXQ5 ANOGA	Q7pxq5 anopheles g	202	32	76.2	392	2	Q9YH45 MYXGL	Q9yh45 myxine glut
130	33	78.6	555	2	Q8WY9 9CAUD	Q8wy9 cyanophag	203	32	76.2	397	2	Q94JQ9 ARATH	Q94jq9 arabidopsis
131	33	78.6	562	2	Q51LQ4 MAGR	Q51lq4 magnaporthe	204	32	76.2	402	2	Q6SSU9 MANSN	Q6ssu9 mantheimia
132	33	78.6	577	2	Q7NEN1 MYCGA	Q7nen1 mycoplasma	205	32	76.2	409	2	P73556 SYNY3	P73556 synchocyst
133	33	78.6	593	2	Q6CKF5 KLULA	Q6ckf5 kluyveromyc	206	32	76.2	411	2	Q9KT34 VIBCH	Q9kt34 vibrio chol
134	33	78.6	637	2	Q7VAE2 PROMA	Q7vae2 prochloroc	207	32	76.2	420	1	ODO2 BUCAL	ODO2 buchnera ap
135	33	78.6	667	2	Q6FV41 CANGA	Q6fv41 candida gla	208	32	76.2	428	2	Q82KE3 CHLCV	Q82ke3 chlamydomo
136	33	78.6	673	2	Q61ZU8 CAEBR	Q61zu8 caenorhabdi	209	32	76.2	428	2	Q9PKE7 CHLMU	Q9pke7 chlamydia m
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139	33	78.6	855	2	Q6BTC9 DEBHA	Q6btc9 debaryomyc	212	32	76.2	431	2	Q7JMS5 CAEEL	Q7jms5 caenorhabdi
140	33	78.6	1041	2	Q9PAE0 USTWA	Q9pae0 ustilago ma	213	32	76.2	448	2	Q5NEB8 FRATT	Q5neb8 franciella
141	33	78.6	1166	2	Q5SCY7 HUPLU	Q5scy7 huperzia lu	214	32	76.2	451	2	Q5UW77 WALPM	Q5uw77 halorcula
142	33	78.6	1233	2	Q57261 9TRYP	Q57261 trypanosoma	215	32	76.2	453	2	Q73P24 WALPM	Q73p24 wolbachia p
143	33	78.6	1566	2	Q8J230 USTWA	Q8j230 ustilago ma	216	32	76.2	454	2	O5LH38 BACFR	O5lh38 bacteroides
144	33	78.6	1568	2	Q4P6K5 USTWA	Q4p6k5 ustilago ma	217	32	76.2	460	2	O64XZ5 BACFR	O64xz5 bacteroides
145	33	78.6	1665	2	Q5SCY7 HUPLU	Q5scy7 huperzia lu	218	32	76.2	460	2	O8A169 BACTN	O8a169 bacteroides
146	33	78.6	1668	2	Q5JYM51 CAEEL	Q5jym51 caenorhabdi	219	32	76.2	462	2	Q6NFB8 CORDI	Q6nfb8 cornebacte
147	33	78.6	1895	2	Q8MM09 CAEBR	Q8mm09 caenorhabdi	220	32	76.2	464	2	Q5E5Y7 VIBF1	Q5e5y7 vibrio fisc
148	33	78.6	1896	2	Q60222 CAEBR	Q60222 caenorhabdi	221	32	76.2	464	2	Q8GF15 EDWTA	Q8gf15 edwardsiell
149	33	78.6	1898	2	Q9TVI2 CAEEL	Q9tvi2 caenorhabdi	222	32	76.2	464	2	Q97IG7 CLOAB	Q97ig7 clostridium
150	33	78.6	3043	2	Q5AWI2 EMENI	Q5awi2 aspergillus	223	32	76.2	479	2	Q9SKY1 ARATH	Q9sky1 arabidopsis
151	33	76.2	49	2	Q49852 MYCLE	Q49852 mycobacteri	224	32	76.2	505	2	Q6ZD63 ORYSA	Q6zd63 oryza sativ
152	33	76.2	83	2	Q5W2N4 SULIS	Q5w2n4 sulfolobus	225	32	76.2	511	1	RRB1 YEAST	RRB1 schizosacch
153	33	76.2	100	2	Q7TWH8 MYCBO	Q7twh8 mycobacteri	226	32	76.2	512	2	O13985 SCHPO	O13985 candida gla
154	33	76.2	100	2	Q6Z61 MYCTU	Q6z61 mycobacteri	227	32	76.2	512	2	Q6FN01 CANGA	Q6fn01 candida gla
155	33	76.2	108	2	Q9CVU7 MYCLE	Q9ccv7 mycobacteri	228	32	76.2	521	2	Q759N3 ASHGO	Q759n3 ashbya goss
156	33	76.2	108	1	Y826 RICFR	Q9ccv7 rickettsia	229	32	76.2	523	2	Q6GJN4 KLULA	Q6gjn4 kluyveromyc
157	33	76.2	122	2	Q4G4C4 EDWTA	Q4g4c4 edwardsiell	230	32	76.2	523	2	Q9FUF3 SOYBN	Q9fuf3 glycine max
158	33	76.2	124	2	Q720B0 LISMF	Q720b0 listeria mo	231	32	76.2	590	2	Q7FX24 ANOGA	Q7fx24 anopheles g
159	33	76.2	124	2	Q8Y7G8 LISMO	Q8y7g8 listeria mo	232	32	76.2	633	2	Q418V5 GIBZE	Q418v5 gibberella
160	33	76.2	124	2	Q6G492 BARHE	Q6g492 bartonella	233	32	76.2	728	2	Q4FQY5 9GAMM	Q4fqy5 psychrobact
161	33	76.2	152	2	Q6K3N2 ORYSA	Q6k3n2 oryza sativ	234	32	76.2	738	2	P79190 BOSPR	P79190 bos primige
162	33	76.2	155	2	Q47U01 GEOSL	Q47u01 geobacter s	235	32	76.2	739	1	PECA1 BOVIN	P51866 bos taurus
163	33	76.2	161	2	Q73QF3 TREDE	Q73qf3 treponema s	236	32	76.2	761	2	Q8S3S4 ORYSA	Q8s3s4 oryza sativ
164	33	76.2	173	2	Q44205 AGRHR	Q44205 agrobacteri	237	32	76.2	761	2	Q8MB09 PARUM	Q8mb09 parachlamyd
165	33	76.2	205	2	Q4HKI3 CAMLA	Q4hk13 campylobact	238	32	76.2	794	2	Q70G21 LAICHE	Q70g21 lactobacill
166	33	76.2	230	2	Q7X4H6 PSEPU	Q7x4h6 pseudomonas	239	32	76.2	835	2	Q41865 MAIZE	Q41865 zea mays (m
167	33	76.2	232	1	CSSCI ECO1	P53518 escherichia	240	32	76.2	897	2	Q44828 ARATH	Q44828 arabidopsis
168	33	76.2	232	1	CSSCI ECO1	P53519 escherichia	241	32	76.2	907	2	Q4Q348 LEFMA	Q4q348 leishmania
169	33	76.2	232	2	Q88N18 PSEPK	Q88n18 pseudomonas	242	32	76.2	943	2	Q5F3M0 CHICK	Q5f3m0 gallus gall
170	33	76.2	241	2	Q9HJ99 THEAC	Q9hj99 thermoplas	243	32	76.2	986	2	Q7Q222 ORYSA	Q7q222 oryza sativ
171	33	76.2	292	2	P70915 BACIN	P70915 bacillus in	244	32	76.2	1193	2	Q9CAM1 ARATH	Q9cam1 arabidopsis
172	33	76.2	292	2	Q5ZK93 CHICK	Q5zk93 gallus gall	245	32	76.2	1197	2	Q6YV15 ORYSA	Q6yv15 oryza sativ
173	33	76.2	297	2	Q4MX36 BACCE	Q4mx36 bacillus ce	246	32	76.2	1198	2	Q84XG3 MAIZE	Q84xg3 zea mays (m
174	33	76.2	297	2	Q637Y2 BACCZ	Q637y2 bacillus th	247	32	76.2	1211	2	Q88ZEB LACPL	Q88zeb lactobacill
175	33	76.2	297	2	Q6HFU9 BACHK	Q6hfu9 bacillus th	248	32	76.2	1211	2	Q88ZEB LACPL	Q88zeb lactobacill
176	33	76.2	297	2	Q734B2 BACC1	Q734b2 bacillus ce	249	32	76.2	1275	2	Q6L2P1 PICTO	Q6l2p1 picophilus
177	33	76.2	297	2	Q81AT0 BACC1	Q81at0 bacillus ce	250	32	76.2	1296	2	Q7QJ29 ANOGE	Q7qj29 anopheles g

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:16:43 ; Search time 73.7917 Seconds
(without alignments)
66.928 Million cell updates/sec

Title: US-10-091-135-12
Perfect score: 42
Sequence: 1 IQIKWHK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	92.9	61	2	Q42209 PLABE
2	39	92.9	363	1	DRD1_CARAU
3	38	90.5	240	2	Q97K14_CLOAB
4	37	88.1	162	2	Q7SD13_NEUCR
5	37	88.1	238	2	Q9UZA0_PYRAB
6	37	88.1	492	2	Q7RA59_PLAYO
7	36	85.7	161	2	Q5KU32_CLOCL
8	36	85.7	314	2	Q853P8_9CAUD
9	36	85.7	351	2	Q4UYZ6_XANCP
10	36	85.7	351	2	Q8F534_XANCP
11	36	85.7	428	2	Q19839_CABEL
12	36	85.7	513	2	Q5L1A2_BACFN
13	36	85.7	513	2	Q64ZB5_BACFR
14	36	85.7	513	2	Q8A1P8_BACTN
15	36	85.7	739	2	Q9M5J3_PHAU
16	36	85.7	745	2	Q9ZRV9_CICAR
17	36	85.7	960	2	Q4S4N9_TETNG
18	35	83.3	204	1	VA5_VESFL
19	35	83.3	204	1	VA5_VESFL
20	35	83.3	227	1	VA5_VESVU
21	35	83.3	235	2	Q8SD54_BOVIN
22	35	83.3	240	2	Q8C2X5_MOUSE
23	35	83.3	298	2	Q5UP69_MIMIV
24	35	83.3	393	1	CYH4_MOUSE
25	35	83.3	396	2	Q81YW9_HUMAN
26	35	83.3	408	2	Q571J1_MOUSE
27	35	83.3	473	1	ABGA_CLOLO
28	35	83.3	487	2	Q4NRP0_9DELT
29	35	83.3	639	2	Q4P692_USTMA
30	35	83.3	735	2	Q6ZPT9_MOUSE
31	35	83.3	769	2	Q6LJF4_PHOPR

32	35	83.3	804	2	Q9CJW1_PASMU
33	35	83.3	822	2	Q7TQK8_MOUSE
34	35	83.3	889	2	Q9F2N5_HUMAN
35	35	83.3	961	2	Q8YQV0_ANASP
36	35	83.3	1005	2	Q5SFM8_MOUSE
37	35	83.3	1039	2	Q86NJ2_CAEEL
38	35	83.3	1184	2	Q86NJ3_CAEEL
39	35	83.3	1419	2	Q86NJ4_CAEEL
40	35	83.3	1658	2	Q9B1C1_CAEEL
41	35	83.3	1666	2	Q9XY66_CAEEL
42	34	81.0	61	2	Q9QVU0_9MURI
43	34	81.0	168	1	DRD1_BOVIN
44	34	81.0	178	2	Q4WN56_ASPFU
45	34	81.0	180	1	DRD1_RABIT
46	34	81.0	218	2	Q56HX9_9BACT
47	34	81.0	218	2	Q8GEP5_9BACT
48	34	81.0	218	2	Q9YHA9_MYXGL
49	34	81.0	240	2	Q9YHB0_PETMA
50	34	81.0	244	2	Q8XL70_CLOPE
51	34	81.0	247	2	Q97MD5_CLOAB
52	34	81.0	267	2	Q896N2_CLOTE
53	34	81.0	267	2	Q88U16_LACPL
54	34	81.0	309	2	Q4ST28_TETNG
55	34	81.0	320	2	Q8U676_AGRRT5
56	34	81.0	414	2	Q4SBH5_TETNG
57	34	81.0	429	2	Q84249_CHLTR
58	34	81.0	437	2	Q42316_CYPCA
59	34	81.0	445	2	Q98842_ANGAN
60	34	81.0	445	2	Q98841_ANGAN
61	34	81.0	446	1	DRD1_DIDNA
62	34	81.0	446	1	DRD1_HUMAN
63	34	81.0	446	1	DRD1_MACMU
64	34	81.0	446	1	DRD1_MOUSE
65	34	81.0	446	1	DRD1_PIG
66	34	81.0	446	1	DRD1_RAT
67	34	81.0	446	2	Q6FH34_HUMAN
68	34	81.0	446	2	Q4QRJ0_HUMAN
69	34	81.0	446	2	Q8WMD7_BOVIN
70	34	81.0	446	2	Q42315_CYPCA
71	34	81.0	448	2	Q98844_ANGAN
72	34	81.0	450	2	Q7LZ75_CHICK
73	34	81.0	451	1	DRD1_XENLA
74	34	81.0	457	1	DRD5_XENLA
75	34	81.0	458	2	Q98843_ANGAN
76	34	81.0	458	2	Q4RIQ8_TETNG
77	34	81.0	459	1	DRD1L_FUGRU
78	34	81.0	465	1	DRD1C_XENLA
79	34	81.0	489	1	TRAC2N_MOUSE
80	34	81.0	489	2	Q5M7U8_RAT
81	34	81.0	758	2	Q9D277_MOUSE
82	34	81.0	798	2	Q9U4E1_OXYNO
83	34	81.0	802	2	Q7VM53_HAEDU
84	34	81.0	865	2	Q8L614_ARATH
85	34	81.0	956	2	Q8R004_MOUSE
86	34	81.0	956	2	Q9WVF1_MOUSE
87	34	81.0	984	2	Q6NUW0_BRARE
88	34	81.0	987	2	Q99K74_MOUSE
89	34	81.0	987	2	Q4V8B3_RAT
90	34	81.0	989	1	TS100_HUMAN
91	34	81.0	1194	2	Q5FKY7_ARATH
92	34	81.0	1314	2	Q54S68_DICDI
93	33	78.6	72	2	Q5WRX2_LEGPL
94	33	78.6	92	2	Q7BQ8_XYLFT
95	33	78.6	98	2	Q73S32_MYCPA
96	33	78.6	174	2	Q7R1W8_GIALA
97	33	78.6	183	2	Q7RND8_VIBPA
98	33	78.6	193	1	YK02_YEAST
99	33	78.6	205	2	Q6MPA7_BDEBA
100	33	78.6	228	2	Q6OTD6_CABBR
101	33	78.6	258	2	Q6K2U8_ORYSA
102	33	78.6	295	2	Q5LQ00_SILPO
103	33	78.6	309	2	Q5FJN9_LACAC
104	33	78.6	328	2	Q6UCZ6_9PROT

Q9CJm1	pasteurella
Q7Tqk8	mus musculus
Q92n5	homo sapien
Q8Yqv0	anabaena sp
Q5Sfm8	mus musculus
Q86nj2	caenorhabdi
Q86nj3	caenorhabdi
Q86nj4	caenorhabdi
Q86ic1	caenorhabdi
Q9xy66	caenorhabdi
Q9QVU0	rattus sp.
Q95136	bos taurus
Q4WN56	aspergillus
O02664	oryctolagus
Q56hx9	uncultured
Q8Gep5	myxine glut
Q9Yha9	petromyzon
Q8x170	clostridium
Q97md5	clostridium
Q89en2	clostridium
Q89u16	lactobacill
Q4st28	tetradodon n
Q8u676	agrobacteri
Q4sbh5	tetradodon n
O84249	chlamydia t
O42316	cyprinus ca
Q98842	anguilla an
Q98841	anguilla an
P42288	delphis m
P21728	homo sapien
O77680	macaca mula
Q61616	mus musculus
P50130	sus scrofa
P18901	rattus norv
Q6fh34	homo sapien
Q4qrj0	homo sapien
Q8wmd7	bos taurus
O42315	cyprinus ca
Q98844	anguilla an
Q71z75	gallus gall
P42289	xenopus lae
P42290	xenopus lae
Q98843	anguilla an
Q4riq8	tetradodon n
P53452	fugu rubrip
P42291	xenopus lae
Q91xt6	mus musculus
Q5m7u8	rattus norv
Q9d277	mus musculus
Q9u4e1	oxytricha n
Q7vm53	haemophilus
Q8l614	arabidopsis
Q8r004	mus musculus
Q9wvf1	mus musculus
Q6nuw0	brachydanio
Q99k74	rattus norv
Q4v8b3	h thyrroid h
O75448	h thyrroid h
Q5fk77	arabidopsis
Q54s68	dictyosteli
Q5wrx2	legionella
Q87bq8	xyella fae
Q73e32	mycobacteri
Q7rlw8	gardia lam
Q87nd8	vibrio para
P36042	saccharomyc
Q6otd6	caenorhabdi
Q6k2u8	oryza sativ
Q5lq00	silicibacte
Q5fjn9	lactobacill
Q6uc26	uncultured

103	30	71.4	275	2	T12937	probable phospho	176	29	69.0	172	2	AC2548	hypothetical prote
104	30	71.4	293	2	H70067	transcription regu	177	29	69.0	185	2	E64126	hypothetical prote
105	30	71.4	301	2	A48879	urate oxidase (EC	178	29	69.0	190	2	G64065	probable methylate
106	30	71.4	302	1	A38097	urate oxidase (EC	179	29	69.0	193	2	A86852	hypothetical prote
107	30	71.4	302	2	S75921	hypothetical prote	180	29	69.0	194	2	A11038	probable exonuclea
108	30	71.4	323	2	D82241	conserved hypotet	181	29	69.0	194	2	S10629	hypothetical prote
109	30	71.4	325	2	AB0398	pseudouridylyl sy	182	29	69.0	196	2	AH1149	hypothetical prote
110	30	71.4	330	2	AC0398	asparagine synthet	183	29	69.0	196	2	AH1149	hypothetical prote
111	30	71.4	330	2	F91214	asparagine synthet	184	29	69.0	205	2	JU0223	hypothetical prote
112	30	71.4	330	2	G86060	hypothetical prote	185	29	69.0	208	2	H69950	conserved hypotet
113	30	71.4	335	2	T44270	hypothetical prote	186	29	69.0	211	1	CYRTB3	beta-crystallin B3
114	30	71.4	343	2	JE0409	cellulase (EC 3.2.	187	29	69.0	211	2	B56691	mpal 5'-region hyp
115	30	71.4	343	2	JO0368	cellulase (EC 3.2.	188	29	69.0	213	2	B27898	beta-crystallin B3
116	30	71.4	354	2	AG1354	hypothetical prote	189	29	69.0	213	2	E64145	hypothetical prote
117	30	71.4	354	2	AH1724	hypothetical prote	190	29	69.0	213	2	T00938	hypothetical prote
118	30	71.4	370	2	G84042	hypothetical prote	191	29	69.0	217	2	F64657	probable glucose-6
119	30	71.4	377	2	H82022	protein T27A1.2 [1	192	29	69.0	227	2	G71859	probable dehydroge
120	30	71.4	411	2	H72494	hypothetical prote	193	29	69.0	231	2	I50467	MHC class II beta
121	30	71.4	433	2	S63143	cell division cont	194	29	69.0	232	2	H75422	probable polysacch
122	30	71.4	434	2	G82184	glycerol-3-phospha	195	29	69.0	232	2	H75422	major tegument pro
123	30	71.4	436	2	E72292	glycerol-3-phospha	196	29	69.0	248	2	S71935	probable PTS syate
124	30	71.4	438	2	E84579	hypothetical prote	197	29	69.0	248	2	S71935	probable wbb12 pro
125	30	71.4	447	2	T09414	hypothetical prote	198	29	69.0	259	2	C82153	transposase (06) B
126	30	71.4	465	2	A88868	pectinesterase hom	199	29	69.0	261	2	E70723	adenylyl-sulfate k
127	30	71.4	484	2	JE0261	protein T23B5.3 [1	200	29	69.0	276	1	S47640	nitrate transport
128	30	71.4	490	2	T25147	N-acetylglucosamin	201	29	69.0	276	1	I39928	hypothetical prote
129	30	71.4	579	2	AP2352	hypothetical prote	202	29	69.0	276	2	C86386	deoxyribonuclease
130	30	71.4	609	2	F64045	exonuclease ABC c	203	29	69.0	282	1	ND80A	hypothetical prote
131	30	71.4	657	2	T01301	RNA-directed DNA p	204	29	69.0	291	2	S75654	hypothetical prote
132	30	71.4	801	2	PC6010	RNA helicase Gu -	205	29	69.0	295	2	J01775	dnaJ protein homol
133	30	71.4	822	2	E86601	CHLTR probable pho	206	29	69.0	309	1	S62835	probable membrane
134	30	71.4	822	2	C72023	conserved hypotet	207	29	69.0	309	2	I39342	heat shock protein
135	30	71.4	889	2	T33422	chltr probable pho	208	29	69.0	310	1	B64200	glycosyl transfera
136	30	71.4	945	2	A64714	hypothetical prote	209	29	69.0	318	2	D87506	hypothetical prote
137	30	71.4	945	2	A64714	helicase - Helicob	210	29	69.0	326	2	T38861	UDP-glucose 4-epim
138	30	71.4	946	2	A71805	probable ATP-depen	211	29	69.0	327	2	B97076	serine/threonine-p
139	30	71.4	1036	2	S22383	axolin 1 precursor	212	29	69.0	327	2	H83659	hypothetical prote
140	30	71.4	1123	2	S36846	myosin-binding pro	213	29	69.0	332	2	T33310	hypothetical prote
141	30	71.4	1154	2	T18650	hypothetical prote	214	29	69.0	350	2	T48622	spore coat protein
142	30	71.4	1339	2	A55301	1,3-beta-D-glucan-	215	29	69.0	351	2	I38908	iron(III) ABC tran
143	30	71.4	1506	2	T30886	integumentary muc	216	29	69.0	351	2	A82429	hypothetical prote
144	30	71.4	1684	2	T02367	hypothetical prote	217	29	69.0	359	2	A13268	hypothetical prote
145	30	71.4	1963	1	MWKM	myosin heavy chain	218	29	69.0	364	2	T43467	late expression fa
146	30	71.4	2264	1	GNVVTB	genome polyprotein	219	29	69.0	373	2	T10341	hypothetical prote
147	30	71.4	2481	2	A43908	fibronectin - Afri	220	29	69.0	381	2	S60561	I kappa B-like pro
148	30	71.4	2517	2	T20566	hypothetical prote	221	29	69.0	386	2	S72168	dopamine receptor
149	30	71.4	5107	2	T29144	partial CDS - Caen	222	29	69.0	387	2	T32929	3-oxoacyl-acyl-ca
150	30	71.4	5107	2	T29144	titin, cardiac mus	223	29	69.0	388	2	AG3341	ATP-gated ion chan
151	30	71.4	26926	1	G36852	hypothetical prote	224	29	69.0	388	2	JC6137	interleukin-1 rece
152	29	69.0	74	2	B72169	A45R protein - var	225	29	69.0	398	2	S17428	hypothetical prote
153	29	69.0	76	2	B80648	cation transport r	226	29	69.0	401	2	T42655	cytochrome P450 -
154	29	69.0	76	2	B90844	cation transport r	227	29	69.0	403	2	S57646	cytochrome P450 -
155	29	69.0	76	2	A85702	cation transport r	228	29	69.0	403	2	B87513	A39R protein - vac
156	29	69.0	76	2	F64868	conserved hypotet	229	29	69.0	403	2	E45221	hypothetical prote
157	29	69.0	81	2	T37233	hypothetical prote	230	29	69.0	421	2	T14773	probable amidohydr
158	29	69.0	81	2	A95908	hypothetical prote	231	29	69.0	423	2	B64079	hypothetical prote
159	29	69.0	94	2	AC1474	hypothetical prote	232	29	69.0	435	2	T51533	NADH-ubiquinone ox
160	29	69.0	102	2	S50530	hypothetical prote	233	29	69.0	435	2	T05452	hypothetical prote
161	29	69.0	108	2	JQ2202	hypothetical prote	234	29	69.0	441	2	S29921	hypothetical prote
162	29	69.0	108	2	S21420	general stress pro	235	29	69.0	448	2	C64437	probable urease
163	29	69.0	112	2	A45069	omega-agatoxin IA	236	29	69.0	472	2	H96607	unknown protein F2
164	29	69.0	122	2	AD1092	hypothetical prote	237	29	69.0	472	2	E64120	exodeoxyribonuclea
165	29	69.0	122	2	AC1456	hypothetical prote	238	29	69.0	482	2	E70450	UDP-MurNac-tripept
166	29	69.0	132	2	A11382	hypothetical prote	239	29	69.0	482	2	E70450	UDP-MurNac-tripept
167	29	69.0	132	2	AB1752	V0 protein - Miasa	240	29	69.0	485	1	JC5236	cytochrome P450, C
168	29	69.0	134	2	JQ1355	hypothetical prote	241	29	69.0	498	1	W2M8	E2 protein - human
169	29	69.0	139	2	T49524	hypothetical prote	242	29	69.0	502	2	S36494	E2 protein - human
170	29	69.0	141	2	B81219	beta-crystallin B3	243	29	69.0	510	2	T16146	hypothetical prote
171	29	69.0	146	2	S10089	hypothetical prote	244	29	69.0	510	2	PC4054	cardiac C-protein
172	29	69.0	149	2	T25858	hypothetical prote	245	29	69.0	511	1	S25707	cytochrome P450 4D
173	29	69.0	158	2	S49918	hypothetical prote	246	29	69.0	511	2	E90600	hypothetical prote
174	29	69.0	158	2	AD3583	riboflavin synthas	247	29	69.0	512	2	T13811	hypothetical prote
175	29	69.0	171	2	A10227	hypothetical prote	248	29	69.0	514	1	W2M8	E2 protein - human

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:19:39 ; Search time 11.6667 Seconds
(without alignments)
57.730 Million cell updates/sec

Title: US-10-091-135-12
Perfect score: 42
Sequence: 1 IQIKWHK 7

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	39	92.9	363	2 I50475	dopamine D1 recept
2	38	90.5	240	2 E97002	fusion: transcript
3	37	88.1	238	2 B75033	hypothetical prote
4	36	85.7	428	2 T21450	hypothetical prote
5	35	83.3	204	2 A44583	venom allergen ant
6	35	83.3	204	2 B44583	venom allergen ant
7	35	83.3	961	2 A82270	exonuclease ABC c
8	35	83.3	1666	2 T43169	hypothetical prote
9	34	81.0	247	2 A96932	phosphoserine phos
10	34	81.0	320	2 A13234	hypothetical prote
11	34	81.0	429	2 H71539	probable dihydrol
12	34	81.0	446	1 DXHUD1	dopamine receptor
13	34	81.0	446	2 I47217	dopamine receptor
14	34	81.0	450	2 A55886	dopamine receptor
15	34	81.0	451	2 I51659	dopamine D1A recep
16	34	81.0	457	2 I51660	dopamine D1B recep
17	34	81.0	459	2 A56849	dopamine receptor-
18	34	81.0	465	2 I51661	dopamine D1C recep
19	34	81.0	487	1 DXRTD1	dopamine receptor
20	33	78.6	193	2 S38039	hypothetical prote
21	33	78.6	348	2 T11141	NADH2 dehydrogenas
22	33	78.6	444	2 C55886	dopamine receptor
23	33	78.6	466	1 B43332	glutamate decarbox
24	33	78.6	466	1 S24234	glutamate decarbox
25	33	78.6	466	2 E91178	glutamate decarbox
26	33	78.6	466	2 F86024	glutamate decarbox
27	33	78.6	466	2 G85726	glutamate decarbox
28	33	78.6	466	2 B90891	glutamate decarbox
29	33	78.6	1898	2 T42440	phospholipase C ho

30	78.6	1922	2	T21581	hypothetical prote
31	76.2	49	2	S72972	hypothetical prote
32	76.2	100	2	B70977	probable secreted
33	76.2	104	2	C86954	hypothetical prote
34	76.2	108	2	C71644	hypothetical prote
35	76.2	124	2	AH1238	hypothetical prote
36	76.2	197	2	S19102	CS6 subunits chape
37	76.2	232	1	I83349	translocation prot
38	76.2	307	2	A36955	protein C50H11.9 [
39	76.2	353	2	H88985	CPGglucose 4,6-deh
40	76.2	359	2	AH0766	rfbg protein - Sal
41	76.2	359	2	S15305	hypothetical prote
42	76.2	383	2	T39854	mannose-1-phosphat
43	76.2	389	2	A12230	hypothetical prote
44	76.2	389	2	AC2268	heterocyst envelop
45	76.2	409	2	S77262	hypothetical prote
46	76.2	411	2	B82246	probable transport
47	76.2	420	2	D84965	dihydrolipoamide S
48	76.2	428	2	F81694	pyruvate dehydroge
49	76.2	429	2	B86529	pyruvate dehydroge
50	76.2	429	2	B72095	small chain of NAD
51	76.2	479	2	B97106	hypothetical prote
52	76.2	511	2	S53061	probable chromatin
53	76.2	512	2	T38422	hypothetical prote
54	76.2	905	2	S29329	probable C2H2-type
55	76.2	907	2	T02417	hypothetical prote
56	76.2	1449	2	B84426	hypothetical prote
57	76.2	1555	2	T18688	protein B0272.5 [i
58	76.2	1973	2	G89608	hypothetical prote
59	76.2	1973	2	T18686	B. subtilis faal p
60	76.2	80	2	AC1788	dopamine receptor
61	73.8	156	2	I67751	dopamine receptor
62	73.8	161	2	A48909	venom allergen ant
63	73.8	204	2	C44583	lipopolysaccharide
64	73.8	265	2	AD0972	rfap protein - Esc
65	73.8	265	2	C42535	aspartate-ammonia
66	73.8	330	2	D92230	aspartate-ammonia
67	73.8	332	2	G98094	hypothetical prote
68	73.8	389	2	C96603	probable major tai
69	73.8	390	2	AD1035	neuroblast cell li
70	73.8	417	2	A49129	UDP-N-acetylmuramo
71	73.8	455	2	AD1329	UDP-N-acetylmuramo
72	73.8	455	2	AD1700	dopamine receptor-
73	73.8	463	2	B56849	dopamine receptor
74	73.8	475	2	A41271	dopamine receptor
75	73.8	477	1	DXHUD5	dopamine receptor
76	73.8	486	2	S55886	hypothetical prote
77	73.8	501	2	T28970	hypothetical prote
78	73.8	505	2	S54066	hypothetical prote
79	73.8	521	2	T46250	hypothetical prote
80	73.8	539	2	T38454	methionine-tRNA li
81	73.8	775	2	G64616	penta-phosphate gu
82	73.8	776	2	C71898	guanosine-3',5'-bi
83	73.8	799	2	JH0797	castor protein - f
84	73.8	803	1	AD4070	endopeptidase La (
85	73.8	824	2	AD3098	periplasmic nitrat
86	73.8	834	2	E98188	cell wall-associat
87	73.8	890	2	F69730	hypothetical prote
88	73.8	900	2	T33482	carbamoyl-phosphat
89	73.8	1062	2	H83966	polyketide synthas
90	73.8	2518	2	A12140	heparan sulfate pr
91	73.8	3707	2	S18252	perlecan precursor
92	73.8	4391	2	A38096	protein UNC-89 - C
93	73.8	6642	2	T29757	hypothetical prote
94	71.4	92	2	G82566	pyruvate ferredoxi
95	71.4	186	2	F71857	pyruvate ferredoxi
96	71.4	204	2	D64658	antigen 5 - easter
97	71.4	204	2	B37329	hypothetical prote
98	71.4	210	2	B81343	hypothetical prote
99	71.4	245	2	T19657	hypothetical prote
100	71.4	247	2	T49375	hypothetical prote
101	71.4	264	2	G96978	uncharacterized co
102	71.4	272	2	H83269	hypothetical prote

98	32	76.2	108	5	ABP66786	Human pol	171	31	73.8	265	9	AEA03059	Lipid A b
99	32	76.2	108	7	ADB31669	Human nov	172	31	73.8	266	7	ADC32794	Human nov
100	32	76.2	116	4	AASU7695	Propionib	173	31	73.8	267	8	ADR50904	Protein d
101	32	76.2	116	5	ABM54214	Propionib	174	31	73.8	327	8	ADR50903	Protein d
102	32	76.2	124	5	ABB48097	Listeria	175	31	73.8	330	8	ABU02474	S. pneumo
103	32	76.2	125	5	ABP32249	Human nuc	176	31	73.8	330	8	ADK47108	Streptoco
104	32	76.2	155	4	AM06762	Human fce	177	31	73.8	332	6	ABP81644	Streptoco
105	32	76.2	160	6	ABM69532	Photorhab	178	31	73.8	355	7	ADC86179	Human GPC
106	32	76.2	212	6	ADR14914	Escherich	179	31	73.8	394	2	AAD26726	Human int
107	32	76.2	230	6	ABU40121	Protein e	180	31	73.8	394	2	AAV26928	Human int
108	32	76.2	325	3	ADN27151	Bacterial	181	31	73.8	394	2	AAE00737	Human int
109	32	76.2	332	3	AAAB34831	Gene 27 h	182	31	73.8	394	2	AAE00737	Human int
110	32	76.2	359	2	AAW88341	Salmonell	183	31	73.8	394	6	ABM32681	Human cyt
111	32	76.2	393	3	RAAB27624	Human sec	184	31	73.8	394	6	ABU32680	Human int
112	32	76.2	393	4	AAU01974	Gene #12	185	31	73.8	394	8	ADO20109	Human PRO
113	32	76.2	393	4	RAAB60757	Gene 12 r	186	31	73.8	394	8	ADP54948	Human PRO
114	32	76.2	393	4	RAAB75559	Gene 3 hu	187	31	73.8	394	9	ADY17560	PRO polyp
115	32	76.2	432	2	AAV34903	Chlamydia	188	31	73.8	394	9	ADY17560	PRO polyp
116	32	76.2	438	6	ABU24541	Protein e	189	31	73.8	416	8	ADY08641	Plant ful
117	32	76.2	479	6	ABU23870	Protein e	190	31	73.8	425	5	ABU51616	Helicobac
118	32	76.2	479	7	ADP04571	Bacterial	191	31	73.8	426	8	ADQ67079	Novel hum
119	32	76.2	486	8	ADS51620	Arabidops	192	31	73.8	455	5	ABBA4873	Listeria
120	32	76.2	511	5	AAU82963	S. cerevi	193	31	73.8	455	6	ABU32621	Protein e
121	32	76.2	511	8	ADN15235	Bacterial	194	31	73.8	458	6	ABU18927	Protein e
122	32	76.2	590	8	ADS51622	Soybean C	195	31	73.8	466	8	ADV89674	Streptoco
123	32	76.2	614	8	ADS21284	Bacterial	196	31	73.8	466	8	ADV83075	Streptoco
124	32	76.2	661	2	AAW77048	Human str	197	31	73.8	475	2	AAK31046	Rat D18 d
125	32	76.2	661	3	AAW70078	Human str	198	31	73.8	475	8	ADH69508	Rat dopam
126	32	76.2	928	8	ADY04709	Plant ful	199	31	73.8	475	8	ADO29017	Mouse nov
127	32	76.2	1449	8	ADJ50120	Oil-associ	200	31	73.8	475	8	ADO29017	Mouse nov
128	32	76.2	1902	4	ABE65387	Drosophil	201	31	73.8	477	2	AAK21082	Dopamine
129	32	76.2	3186	7	ADDE47672	Human NOV	202	31	73.8	477	2	AAK79381	Dopamine
130	32	76.2	3186	8	ADJ78942	Human NOV	203	31	73.8	477	2	AAW40802	Human D5
131	32	76.2	3208	7	ADDE47676	Human NOV	204	31	73.8	477	6	ABBS6350	Non-endog
132	32	76.2	3208	8	ADJ78946	Human NOV	205	31	73.8	477	6	ABP81808	Human dop
133	32	76.2	3252	8	ADDE47674	Human NOV	206	31	73.8	477	7	ADK52546	Hematolog
134	32	76.2	3267	7	ADJ78944	Human NOV	207	31	73.8	477	8	ADH69494	Human dop
135	32	76.2	3267	7	ADC99075	Human KPP	208	31	73.8	477	8	ADH69494	Human dop
136	32	76.2	3268	7	ADB79959	Human kin	209	31	73.8	477	8	ADO29016	Human nov
137	32	76.2	36945	9	ADV97835	Murine pr	210	31	73.8	478	9	ADS73655	Human dop
138	31	73.8	41	5	ABJ05469	Human bre	211	31	73.8	478	9	AEA55027	Mouse D(1
139	31	73.8	51	6	ABP78415	N. gonorr	212	31	73.8	479	2	AAK22546	Truncated
140	31	73.8	62	5	ABP05202	Human ORF	213	31	73.8	480	5	ABG78365	Human pro
141	31	73.8	64	4	AAW90119	Human imm	214	31	73.8	480	4	ABG78365	Human pro
142	31	73.8	68	4	AAW16885	Peptide #	215	31	73.8	488	5	ADQ90948	Human 9-0
143	31	73.8	68	4	ABB35866	Peptide #	216	31	73.8	488	7	ADQ9383	Novel pro
144	31	73.8	68	4	ABB35866	Peptide #	217	31	73.8	488	7	ADQ9383	Novel pro
145	31	73.8	68	4	ABB35866	Peptide #	218	31	73.8	488	7	ADQ9383	Novel pro
146	31	73.8	68	4	ABB35866	Peptide #	219	31	73.8	488	7	ADQ9383	Novel pro
147	31	73.8	68	4	ABG50723	Human liv	220	31	73.8	488	7	ADQ9383	Novel pro
148	31	73.8	68	4	ABG50723	Human liv	221	31	73.8	488	7	ADQ9383	Novel pro
149	31	73.8	68	5	ABG38647	Human pep	222	31	73.8	540	8	ADP55887	Human PRO
150	31	73.8	93	9	ADW17339	Eucalyptu	223	31	73.8	566	8	ADP55887	Human PRO
151	31	73.8	128	3	AAAB27972	Human sec	224	31	73.8	574	7	ADQ8614	Novel pro
152	31	73.8	128	6	ADA57613	Gene 9 Hu	225	31	73.8	574	7	ADQ8614	Novel pro
153	31	73.8	128	6	ADA57613	Human sec	226	31	73.8	585	6	ABU17070	Protein e
154	31	73.8	135	8	ADQ66497	Novel hum	227	31	73.8	587	6	ABU17070	Protein e
155	31	73.8	144	4	RAAG74490	Human col	228	31	73.8	587	6	ADA33145	Acinetoba
156	31	73.8	150	8	ADX74424	Plant ful	229	31	73.8	587	6	ADA33145	Acinetoba
157	31	73.8	161	5	ABB98441	Murine do	230	31	73.8	775	2	ABU30872	H. pylori
158	31	73.8	163	2	AAW38654	S. pneumo	231	31	73.8	775	2	ABU30872	H. pylori
159	31	73.8	174	7	ADC86159	Human GPC	232	31	73.8	793	4	ABBS5886	Drosophil
160	31	73.8	178	7	ADC86153	Human GPC	233	31	73.8	803	6	ABU30254	Protein e
161	31	73.8	196	4	AAU19746	Human nov	234	31	73.8	829	8	ADS25721	Bacterial
162	31	73.8	196	5	ABP47966	Human pol	235	31	73.8	834	8	ADS22448	Bacterial
163	31	73.8	196	5	ADCL0928	Human ext	236	31	73.8	850	8	ADS26200	Bacterial
164	31	73.8	197	8	ADX66291	Plant ful	237	31	73.8	850	2	AAW86810	WeraA prot
165	31	73.8	202	4	AAU87113	Novel cen	238	31	73.8	894	2	AAW86810	WeraA prot
166	31	73.8	202	8	ADI54428	Novel hum	239	31	73.8	1062	8	ADBS28298	Bacterial
167	31	73.8	257	4	ABB59453	Drosophil	240	31	73.8	1064	4	ABG14528	Novel hum
168	31	73.8	257	8	ADX80047	Plant ful	241	31	73.8	1076	4	ABG17192	Novel hum
169	31	73.8	265	6	ABU79128	Lipid A b	242	31	73.8	1076	4	ABG18462	Novel hum
170	31	73.8	265	7	ADF43388	Lipid A b	243	31	73.8	1076	4	ABG14909	Novel hum
										1188	8	ADS27535	Bacterial

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:13:51 ; Search time 61.5417 Seconds

(without alignments)
49.977 Million cell updates/sec

Title: US-10-091-135-12

Perfect score: 42

Sequence: 1 IQIKWHK 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A Geneseq 21.*

1: geneseqp1980s.*

2: geneseqp1990s.*

3: geneseqp2000s.*

4: geneseqp2001s.*

5: geneseqp2002s.*

6: geneseqp2003as.*

7: geneseqp2003bs.*

8: geneseqp2004s.*

9: geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	42	100.0	7	AAE28818	Aae28818 Vesputia v
2	37	88.1	238	AAE96339	Aae96339 Putative
3	36	85.7	170	ADX88291	Adx88291 Plant ful
4	36	85.7	222	ADX93307	Adx93307 Plant ful
5	36	85.7	513	ABU20705	Abu20705 Protein e
6	35	83.3	20	AAW35678	Aaw35678 T cell pe
7	35	83.3	49	AAE28814	Aae28814 Vesputia v
8	35	83.3	204	AAW35688	Aaw35688 Vespid an
9	35	83.3	204	AAW45217	Aaw45217 Wild type
10	35	83.3	204	ABG66977	Abg66977 Wasp veno
11	35	83.3	204	ABG66983	Abg66983 Wasp veno
12	35	83.3	204	ABG67104	Abg67104 Wasp veno
13	35	83.3	204	ABG67103	Abg67103 Wasp veno
14	35	83.3	204	ABG67103	Abg67103 Wasp veno
15	35	83.3	204	ABG67103	Abg67103 Wasp veno
16	35	83.3	209	ABM00031	Abm00031 Allergen
17	35	83.3	227	AAE25644	Aae25644 Vesputia s
18	35	83.3	227	AAE13071	Aae13071 Vesputia v
19	35	83.3	227	AAE34893	Aae34893 Wasp alle
20	35	83.3	316	AAW29651	Aaw29651 Human sec
21	35	83.3	503	ABU11748	Abu11748 Human MDD
22	35	83.3	748	ADU74313	Adu74313 PRO polyp
23	35	83.3	804	ABU39533	Abu39533 Protein e
24	35	83.3	1060	AAW79933	Aaw79933 CGDD-8, I

25	34	81.0	23	6	ABB82886	Abb82886 Dopamine
26	34	81.0	246	3	AAE43752	Aae43752 Human can
27	34	81.0	373	2	AAE48703	Aae48703 G-protein
28	34	81.0	373	2	AAW02675	Aaw02675 G-protein
29	34	81.0	382	5	ABG75676	Abg75676 Human DIA
30	34	81.0	382	8	ADO28784	Ado28784 Arresterin
31	34	81.0	382	9	ADX44603	Adx44603 Chimeric
32	34	81.0	382	9	ADY83833	Ady83833 G protein
33	34	81.0	382	9	AEAL3738	Aeal3738 Human DIA
34	34	81.0	382	9	AAE13738	Aae13738 Human DIA
35	34	81.0	445	8	ADH69512	Adh69512 Anguilla
36	34	81.0	446	2	AAE15498	Aae15498 Human dop
37	34	81.0	446	2	AAE15499	Aae15499 Rat dopam
38	34	81.0	446	2	AAE38364	Aae38364 Human dop
39	34	81.0	446	4	ABB56347	Abb56347 Non-endog
40	34	81.0	446	6	ABP81807	Abp81807 Rat dopam
41	34	81.0	446	6	ABM04785	Abm04785 Human GPC
42	34	81.0	446	7	ADC86175	Adc86175 Human dop
43	34	81.0	446	8	ADH69490	Adh69490 Pig dopam
44	34	81.0	446	8	ADH69516	Adh69516 Human dop
45	34	81.0	446	8	ADH69486	Adh69486 Human dop
46	34	81.0	446	8	ADH69504	Adh69504 Rat dopam
47	34	81.0	446	8	ADH69488	Adh69488 Human dop
48	34	81.0	446	8	ADH69506	Adh69506 Rat dopam
49	34	81.0	446	8	ADH69500	Adh69500 Rhesus ma
50	34	81.0	446	8	ADH69514	Adh69514 Opossum d
51	34	81.0	446	8	ADO29014	Ado29014 Mouse nov
52	34	81.0	446	8	ADO29013	Ado29013 Human nov
53	34	81.0	446	8	ADP54013	Adp54013 Human dop
54	34	81.0	446	8	ADP54013	Adp54013 Human dop
55	34	81.0	447	7	ADH69510	Adh69510 Chicken d
56	34	81.0	450	8	ADH69510	Adh69510 Chicken d
57	34	81.0	487	2	AAE13596	Aae13596 D1 dopam1
58	34	81.0	487	2	AAW09795	Aaw09795 D1 dopam1
59	34	81.0	491	8	ADQ96560	Adq96560 T cell ac
60	34	81.0	500	8	ADY96371	Ady96371 Plant ful
61	34	81.0	500	8	ADY13490	Ady13490 Plant ful
62	34	81.0	756	8	ADU82870	Adu82870 Ligand up
63	34	81.0	976	8	AAU94012	Aau94012 Human pro
64	34	81.0	989	3	AAE69670	Aae69670 Human thy
65	34	81.0	989	3	ADH13191	Adh13191 Human mal
66	34	81.0	989	9	AAE15078	Aae15078 Human pol
67	34	81.0	989	9	AAE01569	Aae01569 Human thy
68	34	81.0	1014	9	ADQ96562	Adq96562 T cell ac
69	33	78.6	72	9	ABE42668	Abe42668 L. pneumo
70	33	78.6	81	4	ABB69930	Abb69930 Drosophil
71	33	78.6	114	5	ABP07815	Abp07815 Human ORF
72	33	78.6	135	5	ABB89648	Abb89648 Human pol
73	33	78.6	149	8	ADP81168	Adp81168 Protein o
74	33	78.6	149	8	ADP81170	Adp81170 Protein o
75	33	78.6	191	4	AAU18706	Aau18706 Renal and
76	33	78.6	191	4	AAU22935	Aau22935 Novel hum
77	33	78.6	191	4	AAU87540	Aau87540 Novel cen
78	33	78.6	191	4	AAU97321	Aau97321 Human pol
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80	33	78.6	341	4	ABB62483	Abb62483 Drosophil
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83	33	78.6	567	7	ABG63751	Abg63751 Klebsiell
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87	33	78.6	1155	4	ABG25739	Abg25739 Novel hum
88	33	78.6	1231	4	ABG24397	Abg24397 Novel hum
89	33	78.6	1231	4	ABG17676	Abg17676 Novel hum
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92	32	76.2	83	7	ADJ36594	Adj36594 InflH immu
93	32	76.2	100	4	AAE35229	Aae35229 M tubercu
94	32	76.2	108	4	AAU18045	Aau18045 Human imm
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96	32	76.2	108	4	ABB10199	Abb10199 Human CBN
97	32	76.2	108	4	ABB95634	Abb95634 Human tes

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121	29	58.0	505	7	US-11-096-568A-853	Sequence 853, App	194	28	56.0	166	7	US-11-132-722-35	Sequence 35, Appl
122	29	58.0	513	7	US-11-096-568A-31200	Sequence 31200, A	195	28	56.0	166	7	US-11-132-722-36	Sequence 36, Appl
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126	29	58.0	539	7	US-11-096-568A-29900	Sequence 29900, A	199	28	56.0	166	7	US-11-132-722-40	Sequence 40, Appl
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149	28	56.0	102	7	US-11-079-463-8109	Sequence 8109, Ap	222	28	56.0	189	7	US-11-147-492-30	Sequence 30, Appl
150	28	56.0	105	7	US-11-087-099-7998	Sequence 7998, Ap	223	28	56.0	201	7	US-11-096-568A-25909	Sequence 25909, A
151	28	56.0	109	7	US-11-188-298-4889	Sequence 4889, Ap	224	28	56.0	212	6	US-10-947-071-5	Sequence 5, Appl
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153	28	56.0	127	6	US-10-467-657-5606	Sequence 5606, Ap	226	28	56.0	213	6	US-10-467-657-5338	Sequence 5338, Ap
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160	28	56.0	166	7	US-11-132-722-2	Sequence 2, Appl	233	28	56.0	259	7	US-11-188-298-8982	Sequence 8982, Ap
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168	28	56.0	166	7	US-11-132-722-10	Sequence 10, Appl	241	28	56.0	311	7	US-11-124-368A-201	Sequence 201, Appl
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170	28	56.0	166	7	US-11-132-722-12	Sequence 12, Appl	243	28	56.0				
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OM protein - protein search, using sw model

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(without alignments)
46.352 Million cell updates/sec

Title: US-10-091-135-11

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Searched: 217505 seqs, 42489236 residues

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Minimum DB seq length: 0

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	39	78.0	191	7	US-11-172-740-1733
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5	33	66.0	190	7	US-11-172-740-1730
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11	33	66.0	191	7	US-11-172-740-1737
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23	33	66.0	2009	6	US-10-374-954-2
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29	32	64.0	366	7	US-11-188-298-4763	Sequence 4763, Ap
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53	30	60.0	199	6	US-10-195-888-588	Sequence 588, App
54	30	60.0	199	6	US-10-195-889-588	Sequence 588, App
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83	30	60.0	912	7	US-11-077-550-116	Sequence 116, App
84	30	60.0	914	7	US-11-077-550-120	Sequence 120, App
85	30	60.0	944	7	US-11-077-550-122	Sequence 122, App
86	30	60.0	950	7	US-11-077-550-118	Sequence 118, App
87	30	60.0	983	6	US-10-511-538-91	Sequence 91, Appl
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SUMMARIES

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109	31	62.0	605	1	US-07-955-905A-24	Sequence 24, Appl	182	29	58.0	137	2	US-09-270-767-36458	Sequence 36458, A
110	31	62.0	685	2	US-09-533-029-76	Sequence 76, Appl	183	29	58.0	137	2	US-09-270-767-51675	Sequence 51675, A
111	31	62.0	774	2	US-09-803-165-34	Sequence 34, Appl	184	29	58.0	138	2	US-09-134-000C-6578	Sequence 6578, Ap
112	31	62.0	921	2	US-09-514-599-2	Sequence 2, Appli	185	29	58.0	166	2	US-08-936-165A-512	Sequence 512, App
113	31	62.0	921	2	US-09-996-024-2	Sequence 2, Appli	186	29	58.0	169	2	US-09-198-452A-1009	Sequence 1009, Ap
114	31	62.0	945	2	US-08-747-562-16	Sequence 16, Appl	187	29	58.0	169	2	US-09-438-185A-940	Sequence 3412, Ap
115	31	62.0	1109	2	US-09-688-188B-88	Sequence 88, Appl	188	29	58.0	178	2	US-09-134-001C-3412	Sequence 5, Appli
116	31	62.0	1109	2	US-09-291-417B-88	Sequence 88, Appl	189	29	58.0	184	1	US-08-991-946A-5	Sequence 6106, Ap
117	31	62.0	1227	2	US-09-710-279-96	Sequence 96, Appl	190	29	58.0	185	1	US-09-949-016-6106	Sequence 18, Appl
118	31	62.0	1229	2	US-09-310-293-2	Sequence 2, Appli	191	29	58.0	185	1	US-08-770-54-18	Sequence 18, Appl
119	31	62.0	1229	2	US-09-579-376-2	Sequence 2, Appli	192	29	58.0	185	2	US-09-579-253-18	Sequence 18, Appl
120	31	62.0	1259	2	US-09-134-001C-3757	Sequence 3757, Ap	193	29	58.0	185	2	US-10-039-112A-18	Sequence 18, Appl
121	30.5	61.0	286	2	US-09-270-767-39650	Sequence 39650, A	194	29	58.0	185	2	US-09-650-324A-18	Sequence 18, Appl
122	30.5	61.0	286	2	US-09-270-767-54867	Sequence 54867, A	195	29	58.0	187	2	US-09-949-016-7805	Sequence 7805, Ap
123	30	60.0	71	2	US-10-176-884-65	Sequence 65, Appl	196	29	58.0	241	2	US-09-489-039A-9561	Sequence 9561, Ap
124	30	60.0	91	2	US-09-248-796A-27122	Sequence 27122, A	197	29	58.0	244	2	US-09-270-767-46826	Sequence 46826, A
125	30	60.0	106	2	US-09-107-532A-5357	Sequence 5357, Ap	198	29	58.0	255	2	US-09-270-767-33375	Sequence 33375, A
126	30	60.0	122	2	US-09-248-796A-20778	Sequence 20778, A	199	29	58.0	255	2	US-09-270-767-48592	Sequence 48592, A
127	30	60.0	129	2	US-10-037-417-32	Sequence 32, Appl	200	29	58.0	273	2	US-09-270-767-48592	Sequence 12294, A
128	30	60.0	142	2	US-09-893-737-172	Sequence 172, App	201	29	58.0	275	2	US-09-543-681A-8196	Sequence 8196, Ap
129	30	60.0	179	2	US-09-583-110-3362	Sequence 3362, Ap	202	29	58.0	303	2	US-09-640-211A-995	Sequence 995, App
130	30	60.0	190	2	US-09-621-976-3899	Sequence 3899, Ap	203	29	58.0	303	2	US-09-248-796A-18543	Sequence 18543, A
131	30	60.0	190	2	US-09-107-433-2841	Sequence 2841, Ap	204	29	58.0	325	2	US-09-270-767-41440	Sequence 41440, A
132	30	60.0	199	2	US-09-621-976-5216	Sequence 5216, Ap	205	29	58.0	332	1	US-08-469-649-2	Sequence 2, Appli
133	30	60.0	199	2	US-10-037-417-102	Sequence 102, App	206	29	58.0	332	2	US-09-347-878-60	Sequence 60, Appl
134	30	60.0	205	2	US-09-248-796A-19681	Sequence 19681, A	207	29	58.0	337	2	US-09-489-039A-13203	Sequence 2, Appli
135	30	60.0	212	2	US-09-248-796A-28147	Sequence 28147, A	208	29	58.0	338	2	US-09-867-932A-2	Sequence 2, Appli
136	30	60.0	219	2	US-09-248-796A-19494	Sequence 19494, A	209	29	58.0	348	1	US-08-997-080-170	Sequence 170, App
137	30	60.0	311	2	US-09-134-000C-3892	Sequence 3892, Ap	210	29	58.0	348	1	US-08-997-362-170	Sequence 170, App
138	30	60.0	343	2	US-09-134-000C-6363	Sequence 6363, A	211	29	58.0	348	2	US-09-095-855-170	Sequence 170, App
139	30	60.0	347	2	US-09-248-796A-19101	Sequence 19101, A	212	29	58.0	348	2	US-09-324-542-170	Sequence 170, App
140	30	60.0	358	2	US-09-784-508-4	Sequence 4, Appli	213	29	58.0	348	2	US-09-205-426-170	Sequence 170, App
141	30	60.0	360	2	US-09-248-796A-17971	Sequence 17971, A	214	29	58.0	352	2	US-09-248-796A-18408	Sequence 18408, A
142	30	60.0	367	2	US-09-902-540-16339	Sequence 16339, A	215	29	58.0	365	2	US-09-949-016-11388	Sequence 11388, A
143	30	60.0	404	2	US-10-321-188-76	Sequence 76, Appl	216	29	58.0	371	2	US-09-252-991A-28793	Sequence 28793, A
144	30	60.0	495	2	US-09-902-540-14402	Sequence 14402, A	217	29	58.0	374	2	US-09-252-991A-18651	Sequence 18651, A
145	30	60.0	500	2	US-10-142-231-61	Sequence 61, Appl	218	29	58.0	375	2	US-09-540-236-2185	Sequence 2185, Ap
146	30	60.0	534	2	US-09-107-532A-6549	Sequence 6549, Ap	219	29	58.0	379	2	US-09-543-681A-7089	Sequence 7089, Ap
147	30	60.0	538	2	US-09-438-185A-1026	Sequence 1026, Ap	220	29	58.0	389	2	US-09-949-016-10069	Sequence 10069, A
148	30	60.0	548	2	US-09-543-681A-6920	Sequence 6920, Ap	221	29	58.0	399	2	US-08-860-519-8	Sequence 8, Appli
149	30	60.0	553	2	US-09-198-452A-1100	Sequence 1100, Ap	222	29	58.0	423	2	US-09-248-796A-20238	Sequence 20238, A
150	30	60.0	574	2	US-09-134-001C-5089	Sequence 5089, Ap	223	29	58.0	425	2	US-09-310-363C-8	Sequence 8, Appli
151	30	60.0	679	2	US-09-489-039A-12307	Sequence 12307, A	224	29	58.0	425	2	US-10-117-015-8	Sequence 8, Appli
152	30	60.0	763	1	US-08-742-753-4	Sequence 4, Appli	225	29	58.0	426	2	US-09-134-000C-4401	Sequence 4401, Ap
153	30	60.0	763	2	US-09-949-016-7023	Sequence 7023, Ap	226	29	58.0	430	2	US-09-310-363C-6	Sequence 6, Appli
154	30	60.0	768	2	US-09-949-016-8429	Sequence 8429, Ap	227	29	58.0	430	2	US-10-117-015-6	Sequence 6, Appli
155	30	60.0	776	2	US-09-165-396-3	Sequence 3, Appli	228	29	58.0	448	2	US-09-543-681A-7245	Sequence 7245, Ap
156	30	60.0	803	2	US-09-543-681A-4312	Sequence 4312, Ap	229	29	58.0	451	2	US-09-307-106-50	Sequence 50, Appl
157	30	60.0	825	2	US-09-489-039A-8469	Sequence 8469, Ap	230	29	58.0	476	2	US-09-949-016-6905	Sequence 6905, Ap
158	30	60.0	829	2	US-09-514-599-6	Sequence 6, Appli	231	29	58.0	485	2	US-10-172-502-18	Sequence 18, Appl
159	30	60.0	829	2	US-09-996-024-6	Sequence 6, Appli	232	29	58.0	490	2	US-09-949-016-6218	Sequence 6218, Ap
160	30	60.0	831	1	US-09-047-026A-4	Sequence 4, Appli	233	29	58.0	501	2	US-09-902-540-12135	Sequence 12135, A
161	30	60.0	844	2	US-09-252-991A-25037	Sequence 25037, A	234	29	58.0	531	2	US-10-104-047-3442	Sequence 3442, Ap
162	30	60.0	857	1	US-07-717-331P-3	Sequence 3, Appli	235	29	58.0	546	2	US-08-860-519-2	Sequence 2, Appli
163	30	60.0	862	2	US-09-346-237-1	Sequence 1, Appli	236	29	58.0	559	2	US-09-248-796A-16391	Sequence 2, Appli
164	30	60.0	905	2	US-09-252-991A-24109	Sequence 24109, A	237	29	58.0	581	2	US-09-331-581-2	Sequence 2, Appli
165	30	60.0	1440	2	US-09-357-251-37	Sequence 37, Appl	238	29	58.0	587	2	US-09-809-665A-59	Sequence 59, Appl
166	30	60.0	1512	2	US-09-443-184-48	Sequence 48, Appl	239	29	58.0	590	2	US-09-605-703B-1558	Sequence 10, Appl
167	30	60.0	2418	2	US-09-949-016-10703	Sequence 10703, A	240	29	58.0	591	2	US-09-861-451A-40	Sequence 40, Appl
168	30	60.0	2509	1	US-08-469-005A-10	Sequence 10, Appl	241	29	58.0	600	2	US-08-860-519-9	Sequence 9, Appli
169	30	60.0	2511	2	US-08-261-907-2	Sequence 2, Appli	242	29	58.0	626	2	US-09-198-452A-839	Sequence 839, App
170	29	58.0	75	2	US-08-852-129-51	Sequence 51, Appl	243	29	58.0	637	2	US-09-438-185A-791	Sequence 791, App
171	29	58.0	78	2	US-09-543-681A-4277	Sequence 4277, Ap	244	29	58.0	646	2	US-09-252-991A-18949	Sequence 18949, A
172	29	58.0	83	2	US-09-621-976-6614	Sequence 6614, Ap	245	29	58.0				
173	29	58.0	91	2	US-09-513-999C-7114	Sequence 7114, Ap	246	29	58.0				

105	35	70.0	548	2	Q7Y45_CRYPV	Q7Y45_cryptospori	178	34	68.0	605	2	Q73IK6_WOLPM	Q73ik6 wolbachia p
106	35	70.0	548	2	Q5CMN4_CRYHO	Q5cmn4 cryptospori	179	34	68.0	616	2	Q53EW3_HUMAN	Q53ew3 homo sapien
107	35	70.0	548	2	Q09542_CABEL	Q09542 caenorhabdi	180	34	68.0	617	2	Q7VQR2_CANBF	Q7vqr2 candidatus
108	35	70.0	588	2	Q9NCM2_PLAVI	Q9ncm2 plasmodium	181	34	68.0	678	2	Q54HJ2_DICDI	Q54hj2 dictyosteli
109	35	70.0	588	2	Q9NCM4_PLAVI	Q9ncm4 plasmodium	182	34	68.0	684	2	Q4IAU9_GIBZE	Q4iau9 gibbrella
110	35	70.0	597	2	Q4W444_HORSE	Q4w444 equus caball	183	34	68.0	686	2	Q7KITV5_DROME	Q7kitv5 drosophila
111	35	70.0	599	2	Q9NCN2_PLAVI	Q9ncn2 plasmodium	184	34	68.0	701	2	Q7MMQJ1_PORGI	Q7mmqj1 porphyromon
112	35	70.0	599	2	Q9NCM5_PLAVI	Q9ncm5 plasmodium	185	34	68.0	720	2	Q7Z2C9_DROME	Q7z2c9 drosophila
113	35	70.0	614	2	Q9NCM9_PLAVI	Q9ncm9 plasmodium	186	34	68.0	720	2	Q9VNX6_DROME	Q9vnx6 arabisopsis
114	35	70.0	627	2	Q938J9_9CAUD	Q938j9 temperate p	187	34	68.0	770	2	Q9MA85_ARATH	Q9ma85 ratcus norv
115	35	70.0	627	2	Q79X11_STRF3	Q79x11 streptococc	188	34	68.0	776	1	ZCC2_RAT	Q8k3y6 ratcus norv
116	35	70.0	627	2	Q8K795_STRP3	Q8k795 streptococc	189	34	68.0	776	2	Q5QUM6_IDILO	Q5qum6 idiomarina
117	35	70.0	685	1	SNWA_DICDI	SNWA dictyosteli	190	34	68.0	784	2	Q6C3M0_YARLI	Q6c3m0 yarrowia li
118	35	70.0	695	2	Q5SDS2_DICDI	Q5sds2 dictyosteli	191	34	68.0	787	2	Q72UQ4_LEPIC	Q72uq4 leptospira
119	35	70.0	730	2	Q8PN69_XANAC	Q8pn69 xanthomonas	192	34	68.0	787	2	Q8F093_LEPIN	Q8f093 leptospira
120	35	70.0	736	2	Q65AC2_HORSE	Q65ac2 equus caball	193	34	68.0	939	2	Q41181_GIBZE	Q41181 gibbrella
121	35	70.0	749	2	Q5GX84_XANAC	Q5gx84 xanthomonas	194	34	68.0	981	2	Q612P7_CABER	Q612p7 caenorhabdi
122	35	70.0	777	2	Q4URY5_XANCP	Q4ury5 xanthomonas	195	34	68.0	1038	2	Q5B8E3_Emeni	Q5b8e2 aspergillus
123	35	70.0	777	2	Q8PBL4_XANCP	Q8pbl4 xanthomonas	196	34	68.0	1042	2	Q54L51_DICDI	Q54l51 dictyosteli
124	35	70.0	931	2	Q4JVF0_CORJK	Q4jvf0 corynebacte	197	34	68.0	1064	2	Q54YR4_ASPFU	Q54yr4 aspergillus
125	35	70.0	997	2	Q4PGV8_USTWA	Q4pgv8 ustilago ma	198	34	68.0	1222	2	Q54YC4_DICDI	Q54yc4 dictyosteli
126	35	70.0	1017	2	Q44055_STYLE	Q44055 stytonychia	199	34	68.0	1619	2	Q13407_MAGGR	Q13407 magnaporthe
127	35	70.0	1036	2	Q6P9K7_MOUSE	Q6p9k7 mus muschula	200	34	68.0	1633	2	Q5CX0_CRYPV	Q5cx0 cryptospori
128	35	70.0	1103	1	PMAL_DUNAC	PMAL dunaliella	201	34	68.0	1503	2	Q7RKR5_PLAYO	Q7rkr5 plasmodium
129	35	70.0	1134	2	Q9NPG3_HUMAN	Q9np3 homo sapien	202	34	68.0	2057	2	Q7R4F0_GIALA	Q7r4f0 giardia lam
130	35	70.0	1134	2	Q9P1P7_HUMAN	Q9p1p7 homo sapien	203	33	66.0	42	2	P79052_SCHPO	P79052 schizosacch
131	35	70.0	1134	2	Q4G0F8_MOUSE	Q4g0f8 mus musculu	204	33	66.0	67	2	Q5QN96_ORYSA	Q5qn96 oryza sativ
132	35	70.0	1431	1	HEXAP_HUMAN	Q96t23 homo sapien	205	33	66.0	73	2	Q646B8_BACFR	Q646b8 bacteroides
133	35	70.0	1480	2	Q9SB63_ARATH	Q9sb63 arabidopsis	206	33	66.0	80	2	Q5JYN9_ORYSA	Q5jyn9 oryza sativ
134	35	70.0	1699	2	Q81IK9_PLAVI	Q81ik9 plasmodium	207	33	66.0	87	2	Q7RT83_PLAYO	Q7rt83 plasmodium
135	35	70.0	1708	2	Q81IK6_PLAVI	Q81ik6 plasmodium	208	33	66.0	87	2	Q7T0E8_ARATH	Q7t0e8 arabidopsis
136	35	70.0	1716	2	Q81IM2_PLAVI	Q81im2 plasmodium	209	33	66.0	109	2	Q5VR42_ORYSA	Q5vr42 oryza sativ
137	35	70.0	1716	2	Q81OK3_PLAVI	Q81ok3 plasmodium	210	33	66.0	111	1	CYC2_AGRIC	P00081 agrobacteri
138	35	70.0	1721	2	Q81IM3_PLAVI	Q81im3 plasmodium	211	33	66.0	112	2	Q6Z6T1_ORYSA	Q6z6t1 oryza sativ
139	35	70.0	1731	2	Q81IL3_PLAVI	Q81il3 plasmodium	212	33	66.0	139	2	Q8U7S0_AGR5	Q8u7s0 agrobacteri
140	35	70.0	1739	2	Q81IL8_PLAVI	Q81il8 plasmodium	213	33	66.0	190	2	Q8LD03_ARATH	Q8ld03 arabidopsis
141	35	70.0	1742	2	Q81IL4_PLAVI	Q81il4 plasmodium	214	33	66.0	190	2	Q9LF15_ARATH	Q9lf15 arabidopsis
142	35	70.0	1749	2	Q81IL7_PLAVI	Q81il7 plasmodium	215	33	66.0	190	2	Q9KF29_BACHD	Q9kf29 bacillus ha
143	35	70.0	1751	2	Q81OG9_PLAVI	Q81og9 plasmodium	216	33	66.0	191	2	Q9CS14_ARATH	Q9cs14 arabidopsis
144	35	70.0	1751	2	Q26194_PLAVI	Q26194 plasmodium	217	33	66.0	191	2	Q9M885_ARATH	Q9m885 arabidopsis
145	35	70.0	1756	2	Q81IM1_PLAVI	Q81im1 plasmodium	218	33	66.0	192	1	RS7_ORYSA	Q81jys oryza sativ
146	35	70.0	1756	2	Q81O58_PLAVI	Q81o58 plasmodium	219	33	66.0	192	1	RS7_SECC	Q9xrt4 secale cere
147	35	70.0	1756	2	Q81O91_PLAVI	Q81o91 plasmodium	220	33	66.0	192	2	Q51K2_TRICUM	Q51k2 triticum ae
148	35	70.0	1763	2	Q81IL2_PLAVI	Q81il2 plasmodium	221	33	66.0	192	2	Q5W6R3_ORYSA	Q5w6r3 oryza sativ
149	35	70.0	228	2	Q7RG88_PLAYO	Q7rg88 mycoplasma	222	33	66.0	205	2	Q6Z786_ORYSA	Q6z786 oryza sativ
150	35	68.0	84	2	Q60B22_MYCHY	Q60b22 mycoplasma	223	33	66.0	210	2	Q9JKC5_MOUSE	Q9jkc5 mus musculu
151	34	68.0	107	2	Q6MB72_PAROW	Q6mb72 parachlamyd	224	33	66.0	220	2	Q8MVB8_IXOSC	Q8m vb8 ixodes scap
152	34	68.0	134	2	Q72V43_LEPIC	Q72v43 leptospira	225	33	66.0	220	2	Q68V26_MOUSE	Q68v26 mus musculu
153	34	68.0	134	2	Q8CXR5_LEPIN	Q8cxr5 leptospira	226	33	66.0	220	2	Q68V27_MOUSE	Q68v27 mus musculu
154	34	68.0	145	2	Q661C3_BORGA	Q661c3 borrelia ga	227	33	66.0	234	2	Q4XE72_PLACH	Q4xe72 plasmodium
155	34	68.0	221	2	Q8GQX1_SELRU	Q8gqx1 selenomonas	228	33	66.0	234	2	Q8C1Q8_MOUSE	Q8c1q8 mus musculu
156	34	68.0	263	2	Q4SLJ1_TETNG	Q4slj1 tetraodon n	229	33	66.0	249	2	Q61E63_RAT	Q61e63 rattus norv
157	34	68.0	266	2	Q48894_MICAE	Q48894 microcystis	230	33	66.0	249	2	Q7Q9W5_ANOGA	Q7q9w5 anopheles g
158	34	68.0	294	2	Q06104_YEAST	Q06104 saccharomyc	231	33	66.0	288	2	Q6Z5D1_CABER	Q6z5d1 caenorhabdi
159	34	68.0	294	2	Q6B2S3_YEAST	Q6b2s3 saccharomyc	232	33	66.0	291	2	Q6YU39_ARYSA	Q6yu39 oryza sativ
160	34	68.0	321	2	Q61YV9_CABER	Q61yv9 caenorhabdi	233	33	66.0	297	2	Q5M8S2_MOUSE	Q5m8s2 mus musculu
161	34	68.0	321	2	Q18648_CAEEL	Q18648 caenorhabdi	234	33	66.0	306	2	Q8WT15_PLACH	Q8wt15 plasmodium
162	34	68.0	333	2	Q60872_CABER	Q60872 caenorhabdi	235	33	66.0	306	2	Q8WT17_PLACH	Q8wt17 plasmodium
163	34	68.0	369	2	Q6XC20_KLUOLA	Q6xc20 kluyveromyc	236	33	66.0	312	2	Q4FN80_9RICK	Q4fn80 candidatus
164	34	68.0	425	1	SYT4_MOUSE	P40749 mus musculu	237	33	66.0	329	2	Q75LD6_ORYSA	Q75ld6 oryza sativ
165	34	68.0	425	1	SYT4_MOUSE	P50232 rattus norv	238	33	66.0	335	2	Q9HW14_PSAE	Q9hw14 pseudomonas
166	34	68.0	443	2	Q6MPA9_PAROW	Q6mpa9 parachlamyd	239	33	66.0	335	2	Q6MC54_PARAW	Q6mc54 parachlamyd
167	34	68.0	458	2	Q5XGK7_XENLA	Q5xgk7 xenopus lae	240	33	66.0	366	2	Q4YHU9_PLABE	Q4yhu9 plasmodium
168	34	68.0	485	2	Q6GZ13_TAXCU	Q6gz13 taxus cuspi	241	33	66.0	366	2	Q6CRJ8_KLUOLA	Q6crj8 kluyveromyc
169	34	68.0	486	2	Q9LHP0_ARATH	Q9lhp0 arabidopsis	242	33	66.0	373	2	Q7SW95_BRARE	Q7sw95 brachydanio
170	34	68.0	490	2	Q17840_CAEEL	Q17840 caenorhabdi	243	33	66.0	381	2	Q8H7G9_ARATH	Q8h7g9 arabidopsis
171	34	68.0	499	2	Q571C5_MOUSE	Q571c5 mus musculu	244	33	66.0	381	2	Q9FKAS_ARYSA	Q9fkas arabidopsis
172	34	68.0	543	2	Q7Q9Y9_ANOGA	Q7q9y9 anopheles g	245	33	66.0	384	2	Q4N2V3_THEPA	Q4n2v3 theileria p
173	34	68.0	550	2	Q59V64_CANAL	Q59v64 candida alb	246	33	66.0	386	2	Q511V4_MAGGR	Q511v4 magnaporthe
174	34	68.0	575	2	Q4Z455_PLABE	Q4z455 plasmodium	247	33	66.0	390	2	Q5NRP0_SOLDE	Q5nrp0 solanum dem
175	34	68.0	577	2	Q5NDB8_CHICK	Q5ndb8 gallus gall	248	33	66.0	391	2	Q7Q5D8_ANOGA	Q7q5d8 anopheles g
176	34	68.0	583	2	Q55C09_DICDI	Q55c09 dictyosteli	249	33	66.0	399	2	Q4P315_USTWA	Q4p315 ustilago ma
177	34	68.0	590	2	Q9LYK7_ARATH	Q9lyk7 arabidopsis	250	33	66.0				

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:16:43 ; Search time 94.875 Seconds
(without alignments)
66.928 Million cell updates/sec

Title: US-10-091-135-11
Perfect score: 50
Sequence: 1 PKKFGSND 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	227	1 VA5_VRSFL	Q05110 vespula vul
2	45	80.0	204	1 VAS_VRSFL	P35783 vespula fla
3	40	80.0	101	2 Q4MKK2_BACCE	Q4mkk2 bacillus ce
4	40	80.0	354	2 Q4MIN9_BACCE	Q4min9 bacillus ce
5	40	80.0	478	2 Q8KYQ6_BACAN	Q8kyq6 bacillus an
6	40	80.0	478	2 Q6EZM1_BACAN	Q6ezm1 bacillus an
7	39	80.0	191	1 RS7_BRAOL	Q9xh45 brassica ol
8	39	78.0	347	2 Q4UFS1_THEAN	Q4ufsl theileria a
9	39	78.0	896	2 Q9FJ23_ARATH	Q9fj23 arabidopsis
10	38	76.0	89	2 Q21332_CABEL	Q21332 caenorhabdi
11	38	76.0	595	2 Q54HF5_DICDI	Q54hf5 dictyosteli
12	37	74.0	204	1 VAS_VRSGE	P35784 vespula ger
13	37	74.0	204	1 VAS_VRSMC	P35780 vespula mac
14	37	74.0	204	1 VAS_VRSPE	P35785 vespula pen
15	37	74.0	373	2 Q71U48_LACCL	Q71u48 lactobacill
16	37	74.0	373	2 Q845A6_LACCL	Q845a6 lactobacill
17	37	74.0	571	2 Q7XE56_ORYSA	Q7xe56 oryza sativ
18	37	74.0	604	1 YJ13_YEAST	P47030 saccharomyc
19	37	74.0	803	2 Q81B35_PLAFA7	Q81b35 plasmodium
20	37	74.0	1659	2 Q5AGQ3_CANAL	Q5agq3 candida alb
21	37	74.0	1661	2 Q5AGC3_CANAL	Q5agc3 candida alb
22	37	74.0	1664	2 INT1_CANAL	P53705 candida alb
23	36	72.0	170	1 RUVC_AGRTS	Q8u9k4 agrobacteri
24	36	72.0	170	1 RUVC_RHIME	Q92m90 rhizobium m
25	36	72.0	223	2 Q98BA4_RHILLO	Q98ba4 rhizobium l
26	36	72.0	310	1 ODCL_YEAST	Q03028 saccharomyc
27	36	72.0	315	2 Q41DZ5_GIBZE	Q41dz5 gibberella
28	36	72.0	478	1 T231C_BACTH	P12250 bacillus th
29	36	72.0	478	1 T231D_BACTH	Q05501 bacillus th
30	36	72.0	478	2 Q5MRA5_BACTK	Q5mra5 bacillus th
31	36	72.0	482	2 Q5DT40_BACTU	Q5dt40 bacillus th

32	36	72.0	537	1	Z029_XENLA	P18748 xenopus lae
33	36	72.0	543	2	Q4N480_THEPA	Q4n480 theileria p
34	36	72.0	552	2	Q4UFB2_THEAN	Q4ufb2 theileria a
35	36	72.0	557	2	Q5XWL7_SOLTU	Q5xwl7 solanum tub
36	36	72.0	742	2	Q9WAU7_9COMO	Q9wau7 broad bean
37	36	72.0	742	2	Q9WAU8_9COMO	Q9wau8 broad bean
38	36	72.0	742	2	Q9WAU9_9COMO	Q9wau9 broad bean
39	36	72.0	742	2	Q4WR8_9COMO	Q4wr8 broad bean
40	36	72.0	824	2	Q12663_9COMO	Q12663 broad bean
41	36	72.0	885	1	CYK3_YEAST	Q07533 saccharomyc
42	36	72.0	937	2	Q9WDH0_9COMO	Q9wdh0 broad bean
43	36	72.0	937	2	Q9Q202_9COMO	Q9q2q2 broad bean
44	36	72.0	1064	2	Q997C9_9COMO	Q997c9 broad bean
45	36	72.0	1064	2	Q91R41_9COMO	Q91r41 broad bean
46	36	72.0	1064	2	Q91ZU4_9COMO	Q91zu4 broad bean
47	36	72.0	1064	2	Q9YM09_9COMO	Q9ym09 broad bean
48	36	72.0	1064	2	Q9Z006_9COMO	Q9z006 patchouli m
49	36	72.0	1064	2	Q9WAU6_9COMO	Q9wau6 broad bean
50	36	72.0	1065	2	Q9Q2Q3_9COMO	Q9q2q3 broad bean
51	36	72.0	1482	2	Q8I3M8_PLAFA7	Q8i3m8 plasmodium
52	36	72.0	2515	2	O77365_PLAFA7	O77365 plasmodium
53	35	70.0	53	2	Q81B17_BACCR	Q81b17 bacillus ce
54	35	70.0	82	2	Q99MC1_RAT	Q99mc1 rattus norv
55	35	70.0	83	2	Q6GR61_XENLA	Q6gr61 xenopus lae
56	35	70.0	83	2	Q8P8B1_XENTR	Q8p8b1 xenopus tro
57	35	70.0	83	2	Q7T319_BRARE	Q7t319 brachydanio
58	35	70.0	102	2	Q80VH1_MOUSE	Q80vh1 mus musculu
59	35	70.0	117	2	Q4MIP5_BACCE	Q4mip5 bacillus ce
60	35	70.0	165	2	Q95QI9_CAEEL	Q95qi9 caenorhabdi
61	35	70.0	166	2	Q4MFY5_BACCE	Q4mfy5 bacillus ce
62	35	70.0	190	2	Q737L1_BACCI	Q737l1 bacillus ce
63	35	70.0	208	2	Q71T82_BPFI	Q71t82 bacterioph
64	35	70.0	231	2	Q4MNS6_BACCE	Q4mns6 bacillus ce
65	35	70.0	231	2	Q4MUV5_BACCE	Q4muvs6 bacillus ce
66	35	70.0	231	2	Q4MV30_BACCE	Q4mv30 bacillus ce
67	35	70.0	238	2	Q8N0E0_PLAVI	Q8n0e0 plasmodium
68	35	70.0	252	2	Q6XE32_9EUKA	Q6xe32 prymnesium
69	35	70.0	256	2	Q8N0D6_PLAVI	Q8n0d6 plasmodium
70	35	70.0	278	2	Q4MFT3_BACCE	Q4mft3 bacillus ce
71	35	70.0	287	2	Q9ULA6_HUMAN	Q9ula6 homo sapien
72	35	70.0	310	2	Q9ZXS4_BPHH1	Q9zxe4 bacterioph
73	35	70.0	329	2	Q9S6K4_BACTU	Q9s6k4 bacillus th
74	35	70.0	333	2	Q9CV75_MOUSE	Q9cv75 mus musculu
75	35	70.0	334	2	Q9ZSV3_BACTU	Q9zsv3 bacillus th
76	35	70.0	340	1	RPOA_ANTFO	Q85a01 anthoceros
77	35	70.0	344	2	Q13079_HUMAN	Q13079 homo sapien
78	35	70.0	374	2	Q817K5_CAEEL	Q817ks caenorhabdi
79	35	70.0	398	1	Y352_CLOBB	P35838 clostridium
80	35	70.0	418	2	Q60P79_CABBR	Q60p79 caenorhabdi
81	35	70.0	462	1	NIEK_METMP	P71527 methanococc
82	35	70.0	475	2	Q5CI36_CRYHO	Q5ci36 cryptospori
83	35	70.0	477	1	T231F_BACTI	Q02404 bacillus th
84	35	70.0	477	2	Q4R514_MACFA	Q4r514 macaca fasc
85	35	70.0	477	2	Q5MRA6_BACTU	Q5mra6 bacillus th
86	35	70.0	477	2	Q5MYT6_BACTI	Q5myt6 bacillus th
87	35	70.0	477	2	Q5U821_BACTT	Q5u821 bacillus th
88	35	70.0	477	2	Q7AL69_BACTU	Q7al69 bacillus th
89	35	70.0	477	2	Q8RLM1_BACTU	Q8rlm1 bacillus th
90	35	70.0	478	1	T231E_BACTF	Q02403 bacillus th
91	35	70.0	478	2	Q5MRA7_BACTU	Q5mra7 bacillus th
92	35	70.0	478	2	Q5MRA8_BACTF	Q5mra8 bacillus th
93	35	70.0	478	2	Q9X306_BACAN	Q9x306 bacillus an
94	35	70.0	478	2	Q4MI47_BACCE	Q4mi47 bacillus ce
95	35	70.0	478	2	Q4MJ44_BACCE	Q4mj44 bacillus ce
96	35	70.0	482	2	Q4MP37_BACCE	Q4mp37 bacillus ce
97	35	70.0	486	2	Q4QGX4_DEIMA	Q4qgx4 leishmania
98	35	70.0	513	2	Q60VD6_CABBR	Q60vd6 caenorhabdi
99	35	70.0	529	2	Q61L87_CABBR	Q61l87 caenorhabdi
100	35	70.0	536	1	SNW1_HUMAN	Q13573 homo sapien
101	35	70.0	536	2	Q619E2_HUMAN	Q6csl1 mus musculu
102	35	70.0	536	2	Q619E2_HUMAN	Q619e2 homo sapien
103	35	70.0	536	2	Q5CXR9_PONPY	Q5c7r9 pongo pygma
104	35	70.0	548	2	Q5CX17_CRYPV	Q5cx17 cryptospori

103	32	64.0	1428	2	C85079	hypothetical protei	176	30	60.0	265	2	H97324	uncharacterized pr
104	32	64.0	1603	2	A48613	gag/pol polyprotei	177	30	60.0	265	2	S74282	hypothetical prote
105	32	64.0	1893	2	T22661	hypothetical p	178	30	60.0	266	2	T06653	hypothetical prote
106	32	64.0	2437	2	S53811	MBP1 protein - ra	179	30	60.0	269	2	S73999	hypothetical prote
107	31.5	63.0	127	2	AF1253	hypothetical prote	180	30	60.0	269	2	T16487	hypothetical prote
108	31.5	63.0	1706	2	T32495	protein kinase - f	181	30	60.0	284	2	B69945	phage-related prot
109	31	62.0	91	2	S78703	hypothetical prote	182	30	60.0	285	2	G87298	short chain dehydr
110	31	62.0	99	2	S78703	protein YBL091C-a	183	30	60.0	302	2	E97323	probable epimerase
111	31	62.0	160	2	F87399	hypothetical prote	184	30	60.0	330	2	B65179	ribose operon repr
112	31	62.0	204	2	T15295	hypothetical prote	185	30	60.0	330	2	H86061	regulator for rbs
113	31	62.0	207	2	T07332	ribosomal protein	186	30	60.0	330	2	G91215	regulator for rbs
114	31	62.0	210	2	T14734	NS5 protein - sorg	187	30	60.0	330	2	G90256	DNA primase, proba
115	31	62.0	221	2	D91210	probable phosphata	188	30	60.0	332	2	AI0951	ribose operon repr
116	31	62.0	221	2	G86056	probable phosphata	189	30	60.0	355	2	AF1608	branched-chain fat
117	31	62.0	248	2	A39534	floral homeotic pr	190	30	60.0	358	2	JQ1292	hypothetical 39K p
118	31	62.0	257	2	AH1561	molybdate ABC tran	191	30	60.0	406	1	S19531	cytochrome P450 er
119	31	62.0	258	2	T39347	probable tricarbox	192	30	60.0	433	2	T19607	hypothetical prote
120	31	62.0	323	2	AC2481	hypothetical prote	193	30	60.0	440	2	B71293	hypothetical prote
121	31	62.0	325	2	B90023	conserved hypotet	194	30	60.0	448	2	S25324	hypothetical prote
122	31	62.0	330	2	T29640	mitochondrial carr	195	30	60.0	467	2	S41318	glutamate-ammonia
123	31	62.0	331	2	B95902	probable aldoketo	196	30	60.0	476	2	AB3575	hypothetical prote
124	31	62.0	331	2	A61046	ecdysone-induced m	197	30	60.0	492	2	T26502	deoxyribodipyrimid
125	31	62.0	392	2	A99592	hypothetical prote	198	30	60.0	496	2	T52112	hypothetical prote
126	31	62.0	393	2	A49008	paired box transcr	199	30	60.0	499	2	C85022	hypothetical prote
127	31	62.0	457	2	S03961	Ig mu chain C regi	200	30	60.0	513	2	T02002	hypothetical prote
128	31	62.0	469	2	B70201	hypothetical prote	201	30	60.0	514	2	T26501	hypothetical prote
129	31	62.0	478	2	A25122	transposase A - Ba	202	30	60.0	522	2	C96608	hypothetical prote
130	31	62.0	478	2	E29051	transposase B - Ba	203	30	60.0	526	2	F86618	glucose-6-P isomer
131	31	62.0	480	2	T00971	probable disease r	204	30	60.0	526	2	C72005	glucose-6-phosphat
132	31	62.0	501	2	G90534	prolyl-trna-synthe	205	30	60.0	539	2	B81533	phosphoenolpyruvat
133	31	62.0	554	1	NUVKL	hypothetical prote	206	30	60.0	581	2	T16915	hypothetical prote
134	31	62.0	557	1	T26638	beta-conglycinin a	207	30	60.0	590	2	T05329	hypothetical prote
135	31	62.0	571	2	FWSYBA	beta-conglycinin a	208	30	60.0	630	1	BMBY	CBP2 protein - Yea
136	31	62.0	605	1	S20007	probable serine/th	209	30	60.0	650	2	G97100	DNA gyrase B chain
137	31	62.0	605	2	T04837	methyl-accepting c	210	30	60.0	657	2	C97113	serine/threonine p
138	31	62.0	648	2	G82401	auxin response fac	211	30	60.0	662	2	T20570	hypothetical prote
139	31	62.0	652	2	D96621	serine/threonine p	212	30	60.0	662	2	T20570	multifunctional am
140	31	62.0	665	2	T43632	gene bobby sox pro	213	30	60.0	688	2	S46774	hypothetical prote
141	31	62.0	728	2	T08431	serine/threonine p	214	30	60.0	736	2	T25447	hypothetical prote
142	31	62.0	769	2	T43630	hypothetical prote	215	30	60.0	751	2	JC8057	phospholipase C (E
143	31	62.0	792	2	D64343	hypothetical prote	216	30	60.0	776	2	T02565	disease resistance
144	31	62.0	795	2	T33673	hypothetical prote	217	30	60.0	789	2	T28714	lep4 protein - fis
145	31	62.0	798	2	T28013	hypothetical prote	218	30	60.0	789	2	T28714	hypothetical prote
146	31	62.0	881	2	C82516	hypothetical prote	219	30	60.0	803	2	AG0523	glucose dehydrogen
147	31	62.0	903	2	G82516	hypothetical prote	220	30	60.0	803	2	B82099	surface antigen VC
148	31	62.0	919	2	S45298	retinoblastoma-ass	221	30	60.0	831	2	S39835	hypothetical prote
149	31	62.0	945	2	S48369	26S proteasome reg	222	30	60.0	838	2	A32262	fatty-acid synthas
150	31	62.0	1007	2	T42219	alpha-mannosidase	223	30	60.0	846	2	F83388	hypothetical prote
151	31	62.0	1075	2	T27623	hypothetical prote	224	30	60.0	854	2	T14377	S-receptor kinase
152	31	62.0	1080	2	T27622	hypothetical prote	225	30	60.0	907	2	A86460	99.9K hypothetical
153	31	62.0	1229	2	F90040	respiratory nitrat	226	30	60.0	967	2	AH2660	isooleucyl-tRNA syn
154	31	62.0	1254	2	T30855	multidrug resistat	227	30	60.0	967	2	F97442	isooleucyl-tRNA syn
155	31	62.0	1835	2	S46082	urea carboxylase (228	30	60.0	1020	1	WZ8E85	gene 23 protein -
156	30.5	61.0	509	2	T37593	hypothetical prote	229	30	60.0	1021	2	T42566	segment protein 2
157	30.5	61.0	732	2	S46352	env polyprotein -	230	30	60.0	1026	2	T51579	cellulose synthase
158	30	60.0	79	2	A82667	single-stranded DN	231	30	60.0	1131	2	S34213	H+-exporting ATPas
159	30	60.0	118	2	D82777	type 4 fimbriae as	232	30	60.0	1245	2	G88104	protein F40S12.2 (
160	30	60.0	148	2	C82799	single-stranded DN	233	30	60.0	1245	2	T31953	hypothetical prote
161	30	60.0	151	2	H82654	single-stranded DN	234	30	60.0	1276	2	S11455	botulinum neurotox
162	30	60.0	184	2	T43321	ribosomal protein	235	30	60.0	1285	2	S70582	botulinum neurotox
163	30	60.0	189	2	T22034	hypothetical prote	236	30	60.0	1291	2	A94777	botulinum neurotox
164	30	60.0	189	2	T43516	ribosomal protein	237	30	60.0	1355	2	S46431	hypothetical prote
165	30	60.0	189	2	C81428	peptidyl-prolyl ci	238	30	60.0	1440	1	SYHUQT	probable transcrip
166	30	60.0	191	2	S62409	40S ribosomal prot	239	30	60.0	1588	2	T38660	multifunctional am
167	30	60.0	191	2	E84740	hypothetical prote	240	30	60.0	1714	1	S18644	multifunctional am
168	30	60.0	192	2	T40083	40S ribosomal prot	241	30	60.0	1785	2	T21558	hypothetical prote
169	30	60.0	195	2	S31287	ribosomal protein	242	30	60.0	1929	2	T21559	hypothetical prote
170	30	60.0	197	1	S16822	ribosomal protein	243	30	60.0	2505	1	XYRTFA	enoyl-(acyl)-carr
171	30	60.0	202	2	A64480	hypothetical prote	244	30	60.0	2509	2	G01880	fatty-acid synthas
172	30	60.0	218	2	T31642	hypothetical prote	245	30	60.0	2514	2	F81045	hemagglutinin/hemo
173	30	60.0	218	2	T01104	disease resistance	246	30	60.0	2514	2	F81045	peptidyl-prolyl ci
174	30	60.0	231	2	E84965	phosphoglycerate m	247	29.5	59.0	159	2	S82781	hypothetical prote
175	30	60.0	233	2	AD2041	hypothetical prote	248	29	58.0	110	2	S72390	hypothetical prote

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:19:39 ; Search time 15 Seconds
(without alignments)

57.730 Million cell updates/sec

Title: US-10-091-135-11

Perfect score: 50

Sequence: 1 PKKKFSGND 9

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR 80:*

1: Pirl:*

2: Pirl:*

3: Pirl:*

4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	45	90.0	204	A44583	venom allergen ant
2	38	76.0	89	T23462	hypothetical prote
3	37	74.0	204	B37329	antigen 5 - easter
4	37	74.0	204	B44583	venom allergen ant
5	37	74.0	204	C44583	venom allergen ant
6	37	74.0	604	S56027	hypothetical prote
7	37	74.0	1664	T18216	integrin-like prot
8	36	72.0	170	AH3014	Holliday Junction
9	36	72.0	310	S69050	hypothetical prote
10	36	72.0	310	S69050	probable membrane
11	36	72.0	399	E33282	DNA-binding protei
12	36	72.0	478	S25199	transposase - Bac
13	36	72.0	478	C29051	transposase - Ba
14	36	72.0	885	S67660	hypothetical prote
15	36	72.0	2523	T18477	hypothetical prote
16	35	70.0	310	T13528	protein Vm4 (impor
17	35	70.0	344	G01628	protein containing
18	35	70.0	398	H96967	nitrogenase (Bc 1.
19	35	70.0	462	T10094	transposase - Bac
20	35	70.0	477	S25822	hypothetical prote
21	35	70.0	478	C59095	transposase - Bac
22	35	70.0	478	S25821	hypothetical prote
23	35	70.0	561	T16148	hypothetical prote
24	35	70.0	1007	T24643	DNA-directed DNA p
25	35	70.0	1017	T30195	hypothetical prote
26	35	70.0	1480	T05566	major blood-stage
27	35	70.0	1751	A45604	hypothetical prote
28	35	70.0	2504	A57788	enoyl-lacetyl-carrie
29	34	68.0	294	S59774	probable membrane

30	34	68.0	321	2	T24410	hypothetical prote
31	34	68.0	425	2	I59355	synaptotagmin IV -
32	34	68.0	490	2	T21365	hypothetical prote
33	34	68.0	590	2	T48625	pescadillo-like pr
34	34	68.0	1619	2	T30541	ABC1 transport pro
35	33	66.0	87	2	T03993	hypothetical prote
36	33	66.0	111	1	CCRG2	cytochrome c2 - Ag
37	33	66.0	139	2	C99192	cytochrome c2 [imp
38	33	66.0	139	2	AG3094	40S ribosomal prot
39	33	66.0	190	2	T51483	hypothetical prote
40	33	66.0	190	2	B3689	probable 40S ribos
41	33	66.0	191	2	A96526	hypothetical prote
42	33	66.0	335	2	G83088	hypothetical prote
43	33	66.0	437	2	S46796	chromosome segrega
44	33	66.0	458	2	S52594	chromosome segrega
45	33	66.0	673	2	T41768	ACKNPV orf23 - Bom
46	33	66.0	690	2	G72852	copia-like envelop
47	33	66.0	700	2	S09699	bib protein - frui
48	33	66.0	713	2	S84437	probable membrane
49	33	66.0	728	2	F84500	hypothetical prote
50	33	66.0	1159	2	S62562	probable nuclear p
51	33	66.0	1334	2	B6451	probable copia-tyr
52	33	66.0	1356	2	P84486	probable retroelem
53	33	66.0	1432	2	B85431	trichohyalin like
54	33	66.0	1726	2	A39401	merozoite surface
55	33	66.0	1840	1	CHRTM1	sodium channel pro
56	33	66.0	1879	2	T19481	hypothetical prote
57	33	66.0	1951	2	S00320	sodium channel pro
58	33	66.0	1976	2	I56555	sodium channel pro
59	33	66.0	1983	2	A60054	sodium channel alp
60	33	66.0	2005	2	A46269	sodium channel pro
61	33	66.0	2005	2	B25019	sodium channel pro
62	33	66.0	2009	2	A25019	protein-tyrosine-p
63	33	66.0	2302	2	T14328	nucleocapsid prote
64	32	64.0	88	2	A40485	insulin-like growt
65	32	64.0	161	2	C54270	cytochrome C Cj087
66	32	64.0	186	2	D81360	triacylglycerol li
67	32	64.0	264	2	JC4111	casein kinase II (
68	32	64.0	276	2	T49220	hypothetical prote
69	32	64.0	308	2	T26716	hypothetical prote
70	32	64.0	308	2	T30152	hypothetical prote
71	32	64.0	345	2	T06098	sulfate ABC transp
72	32	64.0	351	2	A81132	hypothetical prote
73	32	64.0	366	2	T47360	DNA-binding protei
74	32	64.0	378	2	T06512	hypothetical prote
75	32	64.0	384	2	S76163	hypothetical prote
76	32	64.0	403	2	C70385	hypothetical prote
77	32	64.0	417	2	S76586	hypothetical prote
78	32	64.0	465	2	A55518	hypothetical prote
79	32	64.0	524	2	B81678	glucose-6-phosphat
80	32	64.0	524	2	E96494	protein F7F22.8 [i
81	32	64.0	548	2	A81854	glucose-6-phosphat
82	32	64.0	560	2	S41808	glucose-6-phosphat
83	32	64.0	614	2	T16268	hypothetical prote
84	32	64.0	653	2	F75005	aldehyde-ferredoxi
85	32	64.0	653	2	B71157	hypothetical prote
86	32	64.0	675	2	P85071	hypothetical prote
87	32	64.0	701	1	FORVIR	gag polyprotein -
88	32	64.0	701	2	S11454	gag polyprotein -
89	32	64.0	701	2	F48613	gag polyprotein -
90	32	64.0	701	2	F48613	gag polyprotein -
91	32	64.0	701	2	S35430	hypothetical prote
92	32	64.0	740	2	T09480	hypothetical prote
93	32	64.0	758	2	T39628	hypothetical prote
94	32	64.0	774	2	T22309	hypothetical prote
95	32	64.0	787	2	PC1232	copla polyprotein
96	32	64.0	802	2	C83588	probable hydroxama
97	32	64.0	866	2	B85075	probable athlia tr
98	32	64.0	871	2	T45692	receptor-like prot
99	32	64.0	889	2	T47311	hypothetical prote
100	32	64.0	1079	1	T9FVMI	gag-Rml1-env polyP
101	32	64.0	1409	1	OFFFCP	copla polyprotein
102	32	64.0	1409	1	OFFFCP	copla polyprotein

98	33	66.0	191	3	AAG08429	Aag08429 Arabidops	171	33	66.0	1951	9	AEA44252	Aea44252 Rat sodiu
99	33	66.0	191	3	AAG34639	Aag34639 Arabidops	172	33	66.0	1951	9	AEA44250	Aea44250 Human SCN
100	33	66.0	191	3	AAG19869	Aag19869 Arabidops	173	33	66.0	1959	6	AAE37322	Aae37322 Human ion
101	33	66.0	192	3	AAG40892	Aag40892 Zea mays	174	33	66.0	1962	5	AAE20511	Aae20511 Human ion
102	33	66.0	192	6	ABP96240	Abp96240 Human nuc	175	33	66.0	1973	5	AAE20516	Aae20516 Human ion
103	33	66.0	194	8	ADY05236	Ady05236 Plant ful	176	33	66.0	1976	7	ADSE57386	Adse57386 Rat Prote
104	33	66.0	194	8	ADX75553	Adx75553 Plant ful	177	33	66.0	1978	2	AAW69361	Aaw69361 Tetradoto
105	33	66.0	195	8	ADX88416	Adx88416 Plant ful	178	33	66.0	1978	9	ADX26338	Adx26338 Novel cel
106	33	66.0	205	8	ADX72834	Adx72834 Plant ful	179	33	66.0	1979	9	AEA44245	Aea44245 Murine so
107	33	66.0	209	8	ADX96710	Adx96710 Plant ful	180	33	66.0	1980	3	AAE23563	Aae23563 Human sod
108	33	66.0	212	8	ADY07237	Ady07237 Plant ful	181	33	66.0	1980	5	AAO14927	Aao14927 Human sod
109	33	66.0	213	8	ADY04691	Ady04691 Plant ful	182	33	66.0	1980	7	ADB78600	Adb78600 Human sod
110	33	66.0	213	8	ADX78346	Adx78346 Plant ful	183	33	66.0	1980	7	ADB78605	Adb78605 Human sod
111	33	66.0	215	8	ADX97096	Adx97096 Plant ful	184	33	66.0	1980	7	ADZ88372	Adz88372 Human SCN
112	33	66.0	216	8	ADX96791	Adx96791 Plant ful	185	33	66.0	1981	7	ABR83185	AbR83185 Human SCN
113	33	66.0	217	5	ABG60158	Abg60158 Human DIT	186	33	66.0	1988	2	AAW69362	Aaw69362 Tetradoto
114	33	66.0	217	6	ABU11632	Abu11632 Human MDD	187	33	66.0	1988	2	AAW69362	Aaw69362 Tetradoto
115	33	66.0	217	6	ADX96954	Adx96954 Plant ful	188	33	66.0	1988	7	ABR83184	AbR83184 Human SCN
116	33	66.0	217	8	ADX78915	Adx78915 Plant ful	189	33	66.0	1988	9	ABE843184	Abe843184 Human vol
117	33	66.0	217	8	ADX96694	Adx96694 Plant ful	190	33	66.0	1999	5	ABO6026	AbO6026 Human sod
118	33	66.0	217	8	ADX96978	Adx96978 Plant ful	191	33	66.0	1999	8	ADU78366	AdU78366 Human vol
119	33	66.0	217	8	ADY04643	Ady04643 Plant ful	192	33	66.0	2000	5	ABO6027	AbO6027 Human sod
120	33	66.0	222	8	ADX75722	Adx75722 Plant ful	193	33	66.0	2000	8	ADK81762	AdK81762 Human Nav
121	33	66.0	233	4	ABU72887	Abu72887 Human/mou	194	33	66.0	2000	8	ADP79541	AdP79541 Human sod
122	33	66.0	233	6	ABU62255	Abu62255 Human/mou	195	33	66.0	2000	8	ADP79541	AdP79541 Human sod
123	33	66.0	233	7	ADC17399	Adc17399 Human/mou	196	33	66.0	2000	9	AEA44248	Aea44248 Human adu
124	33	66.0	314	6	ABU62253	Abu62253 Mouse try	197	33	66.0	2005	4	AAE399676	Aae399676 Human adu
125	33	66.0	309	3	ABO3656	AbO3656 Clone 5 v	198	33	66.0	2005	4	AAE399677	Aae399677 Human neo
126	33	66.0	309	3	ABO3655	AbO3655 Clone 3 v	199	33	66.0	2005	4	AAE399677	Aae399677 Human neo
127	33	66.0	309	3	ABO3657	AbO3657 Clone 6 v	200	33	66.0	2005	5	ABR83627	AbR83627 Human GEF
128	33	66.0	312	7	ADC96303	Adc96303 E. faeciu	201	33	66.0	2005	5	ABR83627	AbR83627 Human GEF
129	33	66.0	314	6	ABU72885	Abu72885 Murine zt	202	33	66.0	2005	7	ADB78604	AdB78604 Human sod
130	33	66.0	314	6	ABU62253	Abu62253 Mouse ser	203	33	66.0	2005	7	ADB78605	AdB78605 Human sod
131	33	66.0	314	7	ADY07377	Ady07377 Mouse ser	204	33	66.0	2005	7	ADC46947	AdC46947 Human SCN
132	33	66.0	366	7	ABO75389	AbO75389 Pseudomon	205	33	66.0	2005	8	ADSE2265	Adse2265 Human sod
133	33	66.0	366	8	ADY08192	Ady08192 Plant ful	206	33	66.0	2005	8	ADY27150	AdY27150 Human SCN
134	33	66.0	368	3	AAG26449	Aag26449 Arabidops	207	33	66.0	2005	9	ADY27147	AdY27147 Human SCN
135	33	66.0	369	3	AAG47270	Aag47270 Arabidops	208	33	66.0	2005	9	ADY27151	AdY27151 Human SCN
136	33	66.0	381	3	AAG47292	Aag47292 Arabidops	209	33	66.0	2005	9	ADY27149	AdY27149 Human SCN
137	33	66.0	381	3	AAG26698	Aag26698 Arabidops	210	33	66.0	2005	9	ADY27149	AdY27149 Human SCN
138	33	66.0	458	6	ABR53834	AbR53834 Protein s	211	33	66.0	2009	4	AAE399674	Aae399674 Human adu
139	33	66.0	458	6	ADK64976	AdK64976 Disease t	212	33	66.0	2009	5	AAE320515	Aae320515 Human ion
140	33	66.0	540	6	ABU24461	Abu24461 Protein e	213	33	66.0	2009	5	ABG69291	AbG69291 Human sod
141	33	66.0	570	4	ABG20671	Abg20671 Novel hum	214	33	66.0	2009	5	ABG69291	AbG69291 Human sod
142	33	66.0	614	8	ADY05411	Ady05411 Plant ful	215	33	66.0	2009	5	ABG69293	AbG69293 Human sod
143	33	66.0	619	8	ADY05478	Ady05478 Plant ful	216	33	66.0	2009	5	ABG69289	AbG69289 Human sod
144	33	66.0	621	5	ADY07025	Ady07025 Plant ful	217	33	66.0	2009	5	ABG69290	AbG69290 Human sod
145	33	66.0	655	5	ABG97460	Abg97460 S. kaniha	218	33	66.0	2009	5	ABG69290	AbG69290 Human sod
146	33	66.0	655	9	ABE12693	Abe12693 Emedlyne	219	33	66.0	2009	5	AAE16776	Aae16776 Human tra
147	33	66.0	655	9	ABE12693	Abe12693 Streptomy	220	33	66.0	2009	7	ADB78599	AdB78599 Human sod
148	33	66.0	696	4	ABB60920	Abb60920 Drosophil	221	33	66.0	2009	7	ADB78599	AdB78599 Human sod
149	33	66.0	702	8	ADG27023	Adg27023 Human OAT	222	33	66.0	2009	7	ADB78594	AdB78594 Human sod
150	33	66.0	702	8	ADM79590	Adm79590 Human liv	223	33	66.0	2009	7	ADB78598	AdB78598 Human sod
151	33	66.0	713	6	ADQ88228	Adq88228 Human 536	224	33	66.0	2009	7	ADB78598	AdB78598 Human SCN
152	33	66.0	713	6	ADR53234	Adr53234 Protein s	225	33	66.0	2009	7	ADR83180	AdR83180 Human SCN
153	33	66.0	713	7	ADK63692	Adk63692 Disease t	226	33	66.0	2009	7	ADSE57563	Adse57563 Human Pro
154	33	66.0	805	6	AAU47293	Aau47293 Propionib	227	33	66.0	2009	8	ADSE57561	Adse57561 Rat Prote
155	33	66.0	805	6	ABM43812	Abm43812 Propionib	228	33	66.0	2009	8	ADSE57561	Adse57561 Mutant SC
156	33	66.0	851	8	ADH41623	Adh41623 Novel hum	229	33	66.0	2009	8	ADSE57561	Adse57561 Mutant SC
157	33	66.0	851	8	AAO18737	Aao18737 Human NOV	230	33	66.0	2009	8	ADSE57561	Adse57561 Mutant SC
158	33	66.0	943	5	ABE93634	AbE93634 Herbicida	231	33	66.0	2009	8	ADSE57561	Adse57561 Mutant SC
159	33	66.0	1510	9	ABE27326	Abe27326 Pinus rad	232	33	66.0	2009	8	ADSE57561	Adse57561 Mutant SC
160	33	66.0	1726	9	ADZ88370	Adz88370 Human SCN	233	33	66.0	2009	8	ADSE57561	Adse57561 Mutant SC
161	33	66.0	1795	7	ADB78596	AdB78596 Human sod	234	33	66.0	2009	8	ADSE57561	Adse57561 Mutant SC
162	33	66.0	1855	7	ADB78597	AdB78597 Human sod	235	33	66.0	2009	8	ADSE57561	Adse57561 Mutant SC
163	33	66.0	1891	9	ADY27145	Ady27145 Human SCN	236	33	66.0	2009	8	ADSE57561	Adse57561 Mutant SC
164	33	66.0	1942	8	ADSE87534	Adse87534 Mutant SC	237	33	66.0	2009	8	ADSE87534	Adse87534 Mutant SC
165	33	66.0	1950	7	ADB78607	AdB78607 Human adu	238	33	66.0	2009	8	ADSE87534	Adse87534 Mutant SC
166	33	66.0	1951	4	AAE399678	Aae399678 Human neo	239	33	66.0	2009	8	ADSE87534	Adse87534 Mutant SC
167	33	66.0	1951	4	AAE399678	Aae399678 Human neo	240	33	66.0	2009	8	ADSE87534	Adse87534 Mutant SC
168	33	66.0	1951	7	ADSE3628	Adse3628 Rat Prote	241	33	66.0	2009	8	ADSE87534	Adse87534 Mutant SC
169	33	66.0	1951	8	ADL06576	Adl06576 Human tum	242	33	66.0	2009	8	ADSE87534	Adse87534 Mutant SC
170	33	66.0	1951	8	ADP79543	Adp79543 Human sod	243	33	66.0	2009	8	ADSE87534	Adse87534 Mutant SC

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QM protein - protein search, using sw model

Run on: April 18, 2006, 11:13:51 ; Search time 79.125 Seconds
(without alignments)
49.977 Million cell updates/sec

Title: US-10-091-135-11
Perfect score: 50
Sequence: 1 PKKFGSND 9

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1980s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	50	100.0	9	AAE28817	Aae28817 Vespula v
2	50	100.0	25	AAW35671	Aaw35671 T cell pe
3	50	100.0	48	AAE28813	Aae28813 Vespula v
4	50	100.0	204	AAW35688	Aaw35688 Vespid an
5	50	100.0	204	AAV45217	Aav45217 Wild type
6	50	100.0	204	ABG66977	Abg66977 Wasp veno
7	50	100.0	204	ABG67052	Abg67052 Wasp veno
8	50	100.0	204	ABG67104	Abg67104 Wasp veno
9	50	100.0	204	ABG67103	Abg67103 Wasp veno
10	50	100.0	204	AAE28820	Aae28820 Vespula v
11	50	100.0	209	ABM00031	Abm00031 Allergen
12	50	100.0	227	AAV25644	Aav25644 Vespula s
13	50	100.0	227	AAE13071	Aae13071 Vespula v
14	50	100.0	227	ADC34893	Adc34893 Wasp alle
15	44	88.0	204	ABG66983	Abg66983 Wasp veno
16	37	74.0	25	AAW35670	Aaw35670 T cell pe
17	37	74.0	62	ABG60195	Abg60195 Human DIT
18	37	74.0	62	ABR41712	AbR41712 Human DIT
19	37	74.0	204	AAW35687	Aaw35687 Vespid an
20	37	74.0	1664	AAW99462	Aaw99462 C.abican
21	37	74.0	1664	AAE19799	Aae19799 Candida a
22	37	74.0	1664	AAU79331	Aau79331 Candida a
23	37	74.0	1664	ADC73265	Adc73265 Yeast Int
24	37	74.0	1664	ADM33264	Adm33264 Candida a

25	36	72.0	223	5	ABP08441	Abp08441 Human ORF
26	36	72.0	310	5	ADS64665	Ads64665 Saccharom
27	36	72.0	310	8	ADS44042	Ads44042 Bacterial
28	36	72.0	885	7	ADKG2184	Adk62184 Disease t
29	35	70.0	34	7	ADB67822	Adb67822 Human lun
30	35	70.0	52	4	AAAI4630	Aai14630 Peptide #
31	35	70.0	52	4	AAAI4630	Aai14630 Peptide #
32	35	70.0	52	4	AAAI4630	Aai14630 Peptide #
33	35	70.0	52	4	AAAI4630	Aai14630 Peptide #
34	35	70.0	52	4	AAAI4630	Aai14630 Peptide #
35	35	70.0	52	4	AAAI4630	Aai14630 Peptide #
36	35	70.0	52	4	AAAI4630	Aai14630 Peptide #
37	35	70.0	52	4	AAAI4630	Aai14630 Peptide #
38	35	70.0	52	4	AAAI4630	Aai14630 Peptide #
39	35	70.0	52	4	AAAI4630	Aai14630 Peptide #
40	35	70.0	146	4	ABG10599	Abg10599 Novel hum
41	35	70.0	183	4	ABG10599	Abg10599 Novel hum
42	35	70.0	500	7	ADC37415	Adc37415 Nuclear f
43	35	70.0	536	7	ADC37417	Adc37417 Nuclear f
44	35	70.0	536	7	ADC37419	Adc37419 Nuclear f
45	35	70.0	536	8	ADU60296	Adu60296 Housekeep
46	35	70.0	613	4	ABG22924	Abg22924 Novel hum
47	35	70.0	666	2	AAW13729	Aaw13729 Herbicide
48	35	70.0	858	5	ABG93619	Abg93619 Herbicide
49	35	70.0	942	4	ABG10600	Abg10600 Novel hum
50	35	70.0	1134	4	AAU28072	Aau28072 Novel hum
51	35	70.0	1134	9	ADX05983	Adx05983 Cyclin-de
52	35	70.0	1398	5	ABG97491	Abg97491 Human NOV
53	35	70.0	1400	4	ABG83348	Abg83348 AAP-2 pro
54	35	70.0	1445	6	ABR41365	AbR41365 Human DIT
55	35	70.0	2504	5	ABP54923	Abp54923 Human fat
56	34	68.0	72	5	ABP38211	Abp38211 Staphyloc
57	34	68.0	72	8	ADS06597	Ads06597 Staphyloc
58	34	68.0	78	4	AAO11095	Aao11095 Human pol
59	34	68.0	290	8	ADX76571	Adx76571 Plant ful
60	34	68.0	384	4	AAW62726	Aaw62726 Borrelia
61	34	68.0	408	4	AAW62737	Aaw62737 Borrelia
62	34	68.0	425	7	ADDE6214	Adde6214 Rat Prote
63	34	68.0	425	7	ADDE6214	Adde6214 Rat Prote
64	34	68.0	425	7	ADDE6214	Adde6214 Rat Prote
65	34	68.0	425	7	ADDE6214	Adde6214 Rat Prote
66	34	68.0	425	7	ADDE6214	Adde6214 Rat Prote
67	34	68.0	550	5	ABP73370	Abp73370 Candida a
68	34	68.0	654	4	ABW63266	Abw63266 Drosophil
69	34	68.0	688	4	ABW63269	Abw63269 Drosophil
70	34	68.0	775	9	AEA04751	Aea04751 CCCH-type
71	34	68.0	793	7	ADC96596	Adc96596 E. faeciu
72	34	68.0	882	6	ADA33945	Ada33945 Acinetoba
73	34	68.0	974	7	ABO74894	AbO74894 Pseudomon
74	34	68.0	1032	8	ADR86313	Adr86313 Aspergill
75	33	66.0	10	4	AAW87510	Aaw87510 Saccharom
76	33	66.0	24	2	AAR78976	Aar78976 Peptide i
77	33	66.0	45	3	AAW58445	Aaw58445 Arabidops
78	33	66.0	59	3	AAW15655	Aaw15655 Arabidops
79	33	66.0	86	3	AAW59326	Aaw59326 Arabidops
80	33	66.0	86	3	AAW59326	Aaw59326 Arabidops
81	33	66.0	86	3	AAW59326	Aaw59326 Arabidops
82	33	66.0	86	3	AAW59326	Aaw59326 Arabidops
83	33	66.0	86	3	AAW59326	Aaw59326 Arabidops
84	33	66.0	86	3	AAW59326	Aaw59326 Arabidops
85	33	66.0	86	3	AAW59326	Aaw59326 Arabidops
86	33	66.0	101	4	AAO01614	Aao01614 Human pol
87	33	66.0	110	3	AAW15654	Aaw15654 Arabidops
88	33	66.0	124	3	AAW41041	Aaw41041 Zea mays
89	33	66.0	139	3	AAW24692	Aaw24692 Plant SDF
90	33	66.0	140	3	AAW24669	Aaw24669 Plant SDF
91	33	66.0	141	3	AAW60995	Aaw60995 Arabidops
92	33	66.0	154	3	AAW41040	Aaw41040 Zea mays
93	33	66.0	170	3	AAW44967	Aaw44967 Zea mays
94	33	66.0	182	3	AAW60994	Aaw60994 Arabidops
95	33	66.0	183	3	AAW60993	Aaw60993 Arabidops
96	33	66.0	190	3	AAW24691	Aaw24691 Plant SDF
97	33	66.0	191	3	AAW24668	Aaw24668 Plant SDF

99	30	53.6	920	7	US-11-087-099-11404	Sequence 11404, A	172	29	51.8	382	7	US-11-096-568A-16256	Sequence 16256, A
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SUMMARIES

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116	33	58.9	417	4	US-10-724-972A-4231	Sequence 4231, Ap	189	32	57.1	296	4	US-10-238-075-893	Sequence 893, App
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157	32	57.1	128	4	US-10-425-114-54977	Sequence 54977, A	230	32	57.1	811	4	US-10-408-765A-797	Sequence 797, App
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160	32	57.1	143	4	US-10-767-701-53614	Sequence 53614, A	233	32	57.1	909	4	US-10-369-493-12826	Sequence 12826, A
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173	32	57.1	197	4	US-10-425-115-315829	Sequence 315829, A	246	32	57.1				

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:28:34 ; Search time 64.625 Seconds
(without alignments)
71.120 Million cell updates/sec

Title: US-10-091-135-10
Perfect score: 56
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA Main:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	56	100.0	202	4	US-10-001-245-117
5	56	100.0	203	4	US-10-001-245-118
6	56	100.0	204	3	US-09-847-208-162
7	56	100.0	204	4	US-10-091-135-16
8	56	100.0	204	4	US-10-091-135-65
9	56	100.0	204	4	US-10-091-135-81
10	56	100.0	204	4	US-10-091-135-39
11	56	100.0	209	3	US-09-957-806A-22
12	56	100.0	210	4	US-10-001-245-214
13	56	100.0	227	3	US-09-847-208-170
14	56	100.0	227	5	US-10-809-689-82
15	56	100.0	227	3	US-09-847-208-163
16	51	91.1	204	3	US-09-847-208-163
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21	44	78.6	204	3	US-09-847-208-165
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23	40	71.4	214	5	US-10-450-763-53985
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25	37	66.1	171	5	US-10-450-763-42507
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27	37	66.1	412	4	US-10-282-122A-42736

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198	63.4	35	3	US-10-001-245-121	Sequence 121, App
91	62.5	35	4	US-10-425-114-45290	Sequence 45290, A
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145	62.5	40	4	US-10-425-115-222493	Sequence 222493, A
145	62.5	41	4	US-10-425-115-222495	Sequence 222495, A
145	62.5	42	4	US-10-425-115-224235	Sequence 224235, A
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179	62.5	44	4	US-10-425-114-52113	Sequence 52113, A
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419	62.5	47	4	US-09-815-242-13330	Sequence 13330, A
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486	62.5	52	5	US-11-097-143-32391	Sequence 32391, A
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914	62.5	54	4	US-10-043-418-2	Sequence 2, Appli
2096	62.5	55	5	US-10-745-237-36	Sequence 36, Appli
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19	60.7	58	4	US-10-982-193-10	Sequence 10, Appli
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89	60.7	63	3	US-10-916-437-4	Sequence 4, Appli
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69	58.9	89	4	US-10-029-386-29121	Sequence 29121, A
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146	58.9	94	4	US-10-437-963-147748	Sequence 147748, A
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103	31	55.4	513	2	US-09-543-681A-4981	Sequence 1981, Ap	176	30	53.6	389	2	US-10-036-507-15	Sequence 15, Appl
104	31	55.4	514	2	US-09-489-039A-10028	Sequence 10028, A	177	30	53.6	389	2	US-10-197-220-112	Sequence 112, App
105	31	55.4	523	2	US-09-489-039A-14269	Sequence 14269, A	178	30	53.6	391	2	US-09-198-452A-737	Sequence 737, App
106	31	55.4	568	2	US-09-134-001C-3768	Sequence 3768, Ap	179	30	53.6	394	2	US-09-391-606-15	Sequence 15, Appl
107	31	55.4	615	2	US-09-198-452A-1037	Sequence 1037, App	180	30	53.6	394	2	US-09-438-185A-697	Sequence 697, App
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131	30	53.6	76	2	US-09-882-434A-16	Sequence 16, Appl	204	30	53.6	660	2	US-09-976-594-787	Sequence 787, App
132	30	53.6	76	2	US-09-882-434A-17	Sequence 17, Appl	205	30	53.6	662	2	US-09-058-489-15	Sequence 15, Appl
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149	30	53.6	256	2	US-09-270-767-45809	Sequence 45809, A	222	30	53.6	959	2	US-09-107-433-4334	Sequence 4334, Ap
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152	30	53.6	282	2	US-09-544-618-18	Sequence 18, Appl	225	30	53.6	1186	2	US-09-248-796A-16183	Sequence 16183, A
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154	30	53.6	298	2	US-09-591-694-2	Sequence 2, Appl	227	30	53.6	1477	2	US-09-482-500A-1	Sequence 1, Appl
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171	30	53.6	356	2	US-08-765-307A-8	Sequence 8, Appl	244	29	51.8	68	2	US-09-967-869A-5	Sequence 5, Appl
172	30	53.6	356	2	US-09-987-614A-8	Sequence 8, Appl	245	29	51.8	89	2	US-09-819-930-2	Sequence 2, Appl
173	30	53.6	367	2	US-09-391-606-16	Sequence 16, Appl	246	29	51.8	89	2		

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QM protein - protein search, using sw model

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59.230 Million cell updates/sec

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Scoring table: BLOSUM62
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Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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108	35	62.5	648	2	Q5YR37	NOCPA	O5yRj7	nocardia fa	181	34	60.7	387	2	Q8TFB2	9HYPO	P29tB2
109	35	62.5	669	2	Q92T65	RHIME	Q82t65	rhizobium m	182	34	60.7	388	1	CUDP_METAN		P29t38
110	35	62.5	714	2	Q8KCK4	CHITE	Q8kck4	chlorobium	183	34	60.7	388	2	Q96UF4	METAN	P29t38
111	35	62.5	729	2	Q6LZY6	METMP	Q6lzy6	methanococc	184	34	60.7	389	2	Q4PDY3	USTMA	Q96uf4
112	35	62.5	753	2	Q8S275	DROME	Q8s275	drosohilla	185	34	60.7	390	2	Q96UF8	METAN	Q96uf8
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114	35	62.5	781	2	Q9L3E8	STROI	Q9l3e8	streptomyce	187	34	60.7	390	2	Q9UUR5	METAN	Q9uUr5
115	35	62.5	791	2	Q9L1E5	STROI	Q9l1e5	streptomyce	188	34	60.7	390	2	Q5MAD3	METAN	Q5mad3
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121	35	62.5	956	2	Q6C49	KLULA	O6c49	kluyveromye	194	34	60.7	401	2	Q5X4W2	LEGPA	O5x4w2
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136	34	60.7	160	1	RT10	MOUSE	O802k0	mus musculus	209	34	60.7	554	1	MBD4	MOUSE	Q4pg17
137	34	60.7	160	2	Q4V9W5	MOUSE	O4v9w5	mus musculus	210	34	60.7	556	1	GLI1	CHICK	Q92zd7
138	34	60.7	162	2	Q5ZYL6	LEGPH	O5zyl6	legionella	211	34	60.7	579	2	Q7MVT5	PORGI	P55978
139	34	60.7	174	2	Q8G3L0	BIFLO	O8g3l0	bifidobacte	212	34	60.7	581	2	Q8ZYM0	PYRAE	Q7mvt5
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143	34	60.7	281	2	Q8TGH1	9HYPO	O8tgh1	cordyceps c	216	34	60.7	622	2	Q62S26	BACLD	Q82eq0
144	34	60.7	281	2	Q8TF95	9HYPO	O8tf95	cordyceps c	217	34	60.7	633	2	Q6SHJ2	BACLD	Q82eq0
145	34	60.7	281	2	Q8TF99	9HYPO	O8tf99	cordyceps c	218	34	60.7	682	1	GRP78	YEAST	Q82eq0
146	34	60.7	284	2	Q4IAD6	GIBZE	O4iad6	gibberella	219	34	60.7	696	2	Q97FR9	CLOAB	Q82eq0
147	34	60.7	286	2	Q727F6	DESUV	O727f6	desulfovibr	220	34	60.7	697	2	Q8EB65	SHRON	Q82eq0
148	34	60.7	290	2	Q88DP9	PSEPK	O88dp9	pseudomonas	221	34	60.7	705	2	Q8XTL2	RALSO	Q82eq0
149	34	60.7	291	2	Q5G598	MAGR	O5g598	magnaporthe	222	34	60.7	720	2	Q5A7N2	CANAL	Q8xtl2
150	34	60.7	291	2	Q61K06	CAERB	O61k06	caenorhabdi	223	34	60.7	726	2	Q72CM5	DESUV	O5a7n2
151	34	60.7	296	2	Q5IOA0	SHIBO	O5iga0	shigella bo	224	34	60.7	756	2	Q8DKB1	SYNEL	Q72cm5
152	34	60.7	298	2	Q62415	CABEL	O62415	caenorhabdi	225	34	60.7	764	2	Q8XTM0	RALSO	Q8dkb1
153	34	60.7	311	1	MCH	HALSA	O9hpd7	halobacteri	226	34	60.7	787	2	Q6CPG3	KLULA	Q8xtm0
154	34	60.7	318	2	Q5XJ57	BRARE	O5xj57	brachydanio	227	34	60.7	788	1	TSR1	YEAST	Q6cpg3
155	34	60.7	319	2	Q93PS4	COMTE	O93ps4	comamonas t	228	34	60.7	818	2	Q5F8S5	NEIG1	Q5f8s5
156	34	60.7	323	2	Q6TR99	METAN	O6tr99	metarhizium	229	34	60.7	857	2	Q8H9R1	9CAUD	Q5f8s5
157	34	60.7	323	2	Q6TR98	METAN	O6tr98	metarhizium	230	34	60.7	861	2	Q4IP83	GIBZE	Q8h9r1
158	34	60.7	323	2	Q6TR96	METAN	O6tr96	metarhizium	231	34	60.7	863	2	Q8XPQ3	RALSO	Q4ip83
159	34	60.7	323	2	Q6TR95	METAN	O6tr95	metarhizium	232	34	60.7	869	2	Q8PD70	USTMA	Q8xpq3
160	34	60.7	323	2	Q6TR94	METAN	O6tr94	metarhizium	233	34	60.7	900	2	Q7P8H2	FUSNV	Q8pd70
161	34	60.7	323	2	Q6TR93	METAN	O6tr93	metarhizium	234	34	60.7	902	2	Q22444	ARATH	Q7p8h2
162	34	60.7	323	2	Q6TR92	METAN	O6tr92	metarhizium	235	34	60.7	926	2	Q515D5	9FELE	Q22444
163	34	60.7	323	2	Q6TR91	METAN	O6tr91	metarhizium	236	34	60.7	928	2	Q89E4	PSEEM	Q515d5
164	34	60.7	323	2	Q6TR90	METAN	O6tr90	metarhizium	237	34	60.7	943	2	Q8D1M6	YERPE	Q89e4
165	34	60.7	323	2	Q6TR89	METAN	O6tr89	metarhizium	238	34	60.7	954	2	Q8D1M6	YERPE	Q8d1m6
166	34	60.7	323	2	Q6TR88	METAN	O6tr88	metarhizium	239	34	60.7	963	2	Q8D1M6	YERPE	Q8d1m6
167	34	60.7	323	2	Q6TR87	METAN	O6tr87	metarhizium	240	34	60.7	970	2	Q4H8Y3	9DEIO	Q8d1m6
168	34	60.7	323	2	Q6TR86	METAN	O6tr86	metarhizium	241	34	60.7	1063	1	XP01	DROME	Q4h8y3
169	34	60.7	323	2	Q6TR85	METAN	O6tr85	metarhizium	242	34	60.7	1169	2	Q9VX45	DROME	Q9v45
170	34	60.7	323	2	Q6TR84	METAN	O6tr84	metarhizium	243	34	60.7	1174	2	Q8MQX9	DROME	Q8mqx9
171	34	60.7	323	2	Q6TR83	METAN	O6tr83	metarhizium	244	34	60.7	1190	2	Q5APK0	CANAL	Q8mqx9
172	34	60.7	323	2	Q9S4R6	VIBCH	O9s4r6	vibrio chol	245	34	60.7	1201	2	Q71RT7	NITWI	Q5apk0
173	34	60.7	346	2	Q94589	9CILI	O94589	lembadion b	246	34	60.7	1201	2	Q71RT8	NITWI	Q71rt7
174	34	60.7	360	2	Q96TU0	METAN	O96tu0	metarhizium	247	34	60.7	1201	2	Q71RT9	9BRAD	Q71rt8
175	34	60.7	360	2	Q96VA2	METAN	O96va2	metarhizium	248	34	60.7	1201	2	Q8CGE3	MOUSE	Q71rt9
176	34	60.7	360	2	Q96TH9	METAN	O96th9	metarhizium	249	34	60.7	1397	2	Q664Z7	YERPS	Q8ceg3
177	34	60.7	360	2	Q96TH9	METAN	O96th9	metarhizium	250	34	60.7	1422	2	Q664Z7	YERPS	Q664z7

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QM protein - protein search, using sw model

Run on: April 18, 2006, 11:16:43 ; Search time 115.958 Seconds
(without alignments)
66.928 Million cell updates/sec

Title: US-10-091-135-10
Perfect score: 56
Sequence: 1 LTGSTAAKYDD 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	204	1 VAS_VESFL	P35783 vespula fla
2	56	100.0	227	1 VAS_VESFU	Q05110 vespula vul
3	51	91.1	204	1 VAS_VESGE	P35784 vespula ger
4	45	80.4	204	1 VAS_VESPE	P35785 vespula pen
5	44	78.6	204	1 VAS_VESMC	P35760 vespula mac
6	41	73.2	309	2 Q428U5 THAAR	Q428u5 thauera chl
7	41	73.2	309	2 Q428U6 9RHO	Q428u6 thauera chl
8	41	73.2	309	2 Q428U8 THAAR	Q428u8 thauera aro
9	41	73.2	309	2 Q428U9 THAAR	Q428u9 thauera chl
10	41	73.2	309	2 Q428V0 9RHO	Q428v0 thauera chl
11	41	73.2	386	2 Q428U4 THAAR	Q428u4 thauera aro
12	40	71.4	787	2 Q9RSU0 DEIRA	Q86sa8 porcellio d
13	39	69.6	146	1 AGH_PORDI	Q41i8 lactobacill
14	39	69.6	487	2 Q4JL18 LACRE	Q9tca5 nephroselm
15	38	67.9	189	2 Q9TCA5_NEPOL	Q53r46 cryptococcu
16	38	67.9	284	2 Q55R46 CRYNE	Q5kf23 cryptococcu
17	38	67.9	284	2 Q5KR23 CRYNE	Q428u4 thauera ael
18	38	67.9	309	2 Q428U4 THASE	Q428u4 thauera chl
19	38	67.9	533	2 Q4RPR4 TETNG	Q428u4 thauera chl
20	38	67.9	685	2 Q4RW7 TETNG	Q428u4 thauera chl
21	38	67.9	985	1 SMCL_ARATH	Q8vy05 arabidopsis
22	37	66.1	165	2 Q6ZNX5 HUMAN	Q6znx5 homo sapien
23	37	66.1	207	2 Q4UM07 RICFE	Q4um07 rickettsia
24	37	66.1	242	2 Q7PBK2 RICSI	Q7pbk2 rickettsia
25	37	66.1	242	2 Q92ID7 RICCN	Q92id7 rickettsia
26	37	66.1	309	2 Q428U7 9RHO	Q428u7 thauera chl
27	37	66.1	342	2 Q98I05 RHIL0	Q98i05 rhizobium 1
28	37	66.1	412	1 YACD_ECOLI	P78105 escherichia
29	37	66.1	476	1 YCTB_SCHPO	P78113 schizosacch
30	37	66.1	480	2 Q8C3E8 MOUSE	Q8c3e8 mus musculus
31	37	66.1	708	2 Q7NK89_GLOVI	Q7nk89 gloeobacter

32	37	66.1	718	2	Q4HD17_9DEIO	Q4hd17 deinococcus
33	37	66.1	744	2	Q928H5_LISIN	Q928h5 listeria in
34	37	66.1	744	2	Q8Y4H8_LISMO	Q8y4h8 listeria mo
35	37	66.1	841	2	Q7VCB3_PROMA	Q7vcb3 prochloroco
36	37	66.1	1724	2	Q4RMC8_TETNG	Q4rmc8 tetraodon n
37	37	66.1	5183	2	Q8TDN5_HUMAN	Q8tdn5 homo sapien
38	37	66.1	5183	2	Q5T4S7_HUMAN	Q5t4s7 homo sapien
39	36	64.3	74	2	Q84235_ORISA	Q84235 oryza sativ
40	36	64.3	102	1	CCAC_AMPCA	P55738 amphidinium
41	36	64.3	142	2	Q82DR7_STRAW	Q82dr7 streptomyce
42	36	64.3	142	2	Q5UQ39_MIMIV	Q5uq39 mimivirus.
43	36	64.3	193	2	Q8KY43_STRCO	Q8ky43 streptomyce
44	36	64.3	193	2	Q82B77_STRAW	Q82b77 streptomyce
45	36	64.3	250	2	Q422M6_PLABE	Q422m6 plasmodium
46	36	64.3	260	1	NQRC_VIBHA	Q9rfv9 vibrio harv
47	36	64.3	294	2	Q8PVU4_METMA	Q8pvu4 methanosarc
48	36	64.3	299	1	PUR7_STRCO	Q9rkl1 streptomyce
49	36	64.3	299	2	Q66G03_PLOIN	Q66g03 plodia inte
50	36	64.3	352	2	Q6ANR4_DESPN	Q6anr4 desulfotale
51	36	64.3	465	2	Q85G88_CYAME	Q85g88 cyanidiosch
52	36	64.3	516	1	PUR9_COREF	Q8frx6 c bifunctio
53	36	64.3	521	1	PUR9_COREF	Q8fr29 c bifunctio
54	36	64.3	524	2	Q8CJ56_STRCO	Q8cj56 streptomyce
55	36	64.3	525	2	Q6NID8_CORDI	Q6nid8 corynebacte
56	36	64.3	721	2	Q8PA53_XANCP	Q8pa53 xanthomonas
57	36	64.3	781	2	Q4LWK6_9BURK	Q4lwk6 burkholderi
58	36	64.3	799	2	Q5KMB5_CRYNE	Q5kmb5 cryptococcu
59	36	64.3	799	2	Q55XW0_CRYNE	Q55xm0 cryptococcu
60	36	64.3	820	2	Q76182_AMPCA	Q76182 amphidinium
61	36	64.3	957	2	Q93781_CAEEL	Q93781 caenorhabdi
62	36	64.3	996	2	Q55HA2_CRYNE	Q55ha2 cryptococcu
63	36	64.3	996	2	Q5K6V8_CRYNE	Q5k6v8 cryptococcu
64	36	64.3	1350	2	Q95Y18_9APIC	Q95y18 plasmodium
65	36	64.3	1350	2	Q7RBM4_PLAYO	Q7rbm4 plasmodium
66	36	64.3	1361	2	Q30524_WOLRE	Q30524 wolinnella r
67	36	64.3	1361	2	Q87083_WOLRE	Q87083 wolinnella r
68	36	64.3	1372	1	CO1A2_MOUSE	Q01149 mus musculu
69	36	64.3	1372	1	CO1A2_RAT	P03466 rattus norv
70	36	64.3	1465	2	Q4UT11_XANCP	Q4ut11 xanthomonas
71	36	64.3	4210	2	Q89J13_BRAJA	Q89j13 bradyrhizob
72	35	62.5	130	2	Q981T9_RHIL0	Q981t9 rhizobium 1
73	35	62.5	145	2	Q9AY76_ORISA	Q9ay76 oryza sativ
74	35	62.5	197	1	NDOC_RICPR	Q9sdh3 rickettsia
75	35	62.5	197	1	Q68X18_RICTY	Q68x18 rickettsia
76	35	62.5	203	2	Q8SR11_ENCCU	Q8sr11 encephalito
77	35	62.5	206	2	Q52DK2_MAGGR	Q52dk2 magnaporthe
78	35	62.5	240	2	Q8JMS0_NUCL	Q8jms0 mamestra co
79	35	62.5	266	2	Q7ULC7_RHOBA	Q7ulc7 rhodopirell
80	35	62.5	272	2	Q4T673_TETNG	Q4t673 tetraodon n
81	35	62.5	299	2	Q4R1X1_TETNG	Q4r1x1 tetraodon n
82	35	62.5	311	2	Q27783_METTH	Q27783 methanobact
83	35	62.5	319	2	Q5G1K1_9BURK	Q5g1k1 comamonas s
84	35	62.5	319	2	Q75T27_PSEOC	Q75t27 pseudomonas
85	35	62.5	335	2	Q80LQ4_NPVAH	Q80lq4 adoxophyes
86	35	62.5	347	2	Q9PHU0_XYLFA	Q9phj0 xyella fas
87	35	62.5	368	2	Q6LBB6_OLICA	Q6lbb6 oligocropha
88	35	62.5	369	2	Q7S111_NEUCR	Q7s111 neurospora
89	35	62.5	390	2	Q52PB4_9DELT	Q52pb4 angiococcus
90	35	62.5	396	1	EFTU_CACR	Q52pb4 angiococcus
91	35	62.5	399	2	Q6A8S9_PROAC	Q6a8s9 caulobacter
92	35	62.5	403	2	Q89S27_BRAJA	Q89s27 bradyrhizob
93	35	62.5	419	1	MURA2_STRPN	Q97qw6 streptococc
94	35	62.5	419	1	MURA2_STRPN	Q8dpv4 streptococc
95	35	62.5	440	2	Q51T97_VAGGR	Q51t97 magnaporthe
96	35	62.5	449	2	Q625A2_CNEBR	Q625a2 caenorhabdi
97	35	62.5	453	2	Q7UES2_RHOBA	Q7ues2 rhodopirell
98	35	62.5	471	1	MOT4_RAT	Q35910 rattus norv
99	35	62.5	476	2	Q4MW79_BACCE	Q4mw79 bacillus ce
100	35	62.5	489	2	Q8IKG5_PLAF7	Q8ikg5 plasmodium
101	35	62.5	504	2	Q4R7J5_WACFA	Q4r7j5 macaca fasc
102	35	62.5	541	1	LNT_BORPA	P61033 bordetella
103	35	62.5	547	1	LNT_BORBR	Q7wmn7 bordetella
104	35	62.5	547	1	LNT_BORPE	P61034 bordetella

103	32	57.1	295	2	F90938	hypothetical prote	176	31	55.4	226	2	H84213	hypothetical prote
104	32	57.1	295	2	B85664	transposase for IS	177	31	55.4	234	2	T49448	hypothetical prote
105	32	57.1	295	2	D90801	hypothetical prote	178	31	55.4	242	2	A86189	protein T2N20.7 [
106	32	57.1	295	2	B85613	probable transposa	179	31	55.4	265	2	G70963	hypothetical prote
107	32	57.1	295	2	B85787	probable transposa	180	31	55.4	269	2	S16671	Dd31 protein - sli
108	32	57.1	295	2	T00315	transposase - Esch	181	31	55.4	283	2	A35935	NADH2 dehydrogenas
109	32	57.1	295	2	B85661	probable transposa	182	31	55.4	316	2	G97148	malonyl CoA-acyl c
110	32	57.1	296	2	A85698	transposase for IS	183	31	55.4	327	2	AG0870	hypothetical prote
111	32	57.1	296	2	A99840	transposase - Esch	184	31	55.4	337	2	AH2591	membrane lipoprote
112	32	57.1	296	2	B67971	probable transposa	185	31	55.4	337	2	B97374	hypothetical prote
113	32	57.1	296	2	A85841	hypothetical prote	186	31	55.4	338	2	T49998	phosphate ABC tran
114	32	57.1	296	2	D91284	hypothetical prote	187	31	55.4	345	2	E84398	outer membrane pro
115	32	57.1	296	2	F90868	hypothetical prote	188	31	55.4	350	2	A82299	x-Pro dipeptidase
116	32	57.1	296	2	D90995	hypothetical prote	189	31	55.4	383	2	AG3312	probable transmemb
117	32	57.1	296	2	E91020	hypothetical prote	190	31	55.4	385	2	G87006	hypothetical prote
118	32	57.1	296	2	A91132	hypothetical prote	191	31	55.4	394	2	F86190	hypothetical prote
119	32	57.1	296	2	F91111	hypothetical prote	192	31	55.4	398	2	T33446	translation elonga
120	32	57.1	296	2	G90998	hypothetical prote	193	31	55.4	399	2	S75862	hypothetical prote
121	32	57.1	296	2	T00240	transposase - Esch	194	31	55.4	399	2	E71169	mannonate dehydrat
122	32	57.1	296	2	E90837	hypothetical prote	195	31	55.4	401	2	A13568	hypothetical prote
123	32	57.1	296	2	C91065	hypothetical prote	196	31	55.4	401	2	E82521	hypothetical prote
124	32	57.1	296	2	H90779	hypothetical prote	197	31	55.4	407	2	S76637	conserved hypothet
125	32	57.1	296	2	C90906	hypothetical prote	198	31	55.4	411	2	A12939	hypothetical prote
126	32	57.1	296	2	A99972	hypothetical prote	199	31	55.4	419	2	F98342	probable flagella-
127	32	57.1	296	2	C90978	hypothetical prote	200	31	55.4	435	2	G75062	hypothetical prote
128	32	57.1	296	2	H85824	IS629 transposase	201	31	55.4	435	2	AD3236	htrA-like protein
129	32	57.1	296	2	S09261	probable transposa	202	31	55.4	449	2	T22777	proteinase DO (EC
130	32	57.1	333	2	JC4308	glyceraldehyde-3-p	203	31	55.4	474	1	I40059	MFS permease (impo
131	32	57.1	338	1	TWMSFB	transforming prote	204	31	55.4	474	2	A13349	hypothetical 51.5k
132	32	57.1	344	2	S34153	mat101-1 protein -	205	31	55.4	475	2	AG2652	hypothetical 51.5k
133	32	57.1	355	2	B69102	hypothetical prote	206	31	55.4	475	2	D97434	conserved hypothet
134	32	57.1	426	2	E96591	hypothetical prote	207	31	55.4	475	2	AE0855	probable 4-hydroxy
135	32	57.1	485	2	E83620	probable amidase p	208	31	55.4	475	2	H91077	probable 4-hydroxy
136	32	57.1	503	2	H87438	tryptophan halogen	209	31	55.4	475	2	T44997	NADH dehydrogenase
137	32	57.1	504	2	F70813	hypothetical prote	210	31	55.4	475	2	A85923	outer capsid prote
138	32	57.1	548	2	T25424	hypothetical prote	211	31	55.4	500	2	AF2325	hypothetical prote
139	32	57.1	553	2	A11395	dipeptide ABC tran	212	31	55.4	526	1	P5XRBT	tubulin-like prote
140	32	57.1	553	2	AD1771	dipeptide ABC tran	213	31	55.4	527	2	T04701	H+-transporting tw
141	32	57.1	585	2	T48513	hypothetical prote	214	31	55.4	562	2	D85439	probable hydrolase
142	32	57.1	614	2	T10862	phasolin G-box bi	215	31	55.4	564	2	A89956	mycodextranase (EC
143	32	57.1	700	2	I40596	glutamate-amonia	216	31	55.4	574	2	S23530	lipid A disacchari
144	32	57.1	721	2	B83237	probable TonB-depe	217	31	55.4	584	2	AI0573	lipid-A-disacchari
145	32	57.1	725	2	C84423	probable ABC trans	218	31	55.4	604	2	C86611	probable peptidase h
146	32	57.1	824	2	T36818	probable secreted	219	31	55.4	604	2	B72014	GRP-binding elonga
147	32	57.1	898	1	D3BP74	DNA-directed DNA p	220	31	55.4	606	2	T35378	beta-lactamase cla
148	32	57.1	935	2	T16489	hypothetical prote	221	31	55.4	612	2	AF1564	integrin beta chai
149	32	57.1	1005	2	C71513	hypothetical prote	222	31	55.4	612	2	AC1208	probable secreted
150	32	57.1	1015	2	T41111	hypothetical App b	223	31	55.4	645	2	S41372	immune inhibitor A
151	32	57.1	1067	1	S62421	endopeptidase La h	224	31	55.4	656	2	S51712	hypothetical prote
152	32	57.1	1178	1	OYBYP	pyruvate carboxyla	225	31	55.4	687	2	S12399	hypothetical prote
153	32	57.1	1253	2	T21065	suppressor of sabl	226	31	55.4	714	2	T15080	beta-lactamase cla
154	32	57.1	1473	2	T13855	zinc metalloprotei	227	31	55.4	715	2	E97245	integrin beta chai
155	32	57.1	1881	2	H95076	variant-specific s	228	31	55.4	735	2	T15306	probable secreted
156	32	57.1	2135	2	T14602	cell wall-associat	229	31	55.4	846	2	A30889	vrIC protein - Dic
157	32	57.1	2331	2	S32920	CPV protein - midg	230	31	55.4	865	2	T34584	hypothetical prote
158	32	57.1	3512	2	T17121	transcription regu	231	31	55.4	875	2	T17382	probable oxidase [
159	31.5	56.2	280	2	H72339	hypothetical prote	232	31	55.4	884	2	T40690	conserved hypothet
160	31.5	56.2	330	2	S70127	hypothetical prote	233	31	55.4	933	2	AG0703	probable oxidase [
161	31	55.4	55	2	P00828	E2/NSI protein (CD	234	31	55.4	933	2	AD3309	conserved hypothet
162	31	55.4	55	2	P00827	E2/NSI protein (CD	235	31	55.4	962	2	D70461	probable oxidase y
163	31	55.4	104	2	B89885	thioredoxin [impor	236	31	55.4	971	2	C71808	conserved hypothet
164	31	55.4	126	2	C69776	hypothetical prote	237	31	55.4	991	2	B64695	type I restriction
165	31	55.4	135	2	H88663	protein C02B10.6 [238	31	55.4	993	2	B46695	type I restriction
166	31	55.4	145	2	T15058	photosystem I prot	239	31	55.4	1018	2	AG0703	probable oxidase [
167	31	55.4	153	2	H86034	hypothetical prote	240	31	55.4	1018	2	B90928	probable oxidase y
168	31	55.4	153	2	G91187	hypothetical prote	241	31	55.4	1018	2	F85776	conserved hypothet
169	31	55.4	153	2	S47817	hypothetical 18.1k	242	31	55.4	1018	2	AH0293	probable iron-sulf
170	31	55.4	155	2	JL0071	alpha-pilin - Mora	243	31	55.4	1023	2	G64926	probable iron-sulf
171	31	55.4	170	2	T35957	NADH2 dehydrogenas	244	31	55.4	1037	2	B59430	carbamoyl-phosphat
172	31	55.4	195	2	S33861	hypothetical prote	245	31	55.4	1043	2	I40377	DNA-binding protei
173	31	55.4	196	2	H69144	hypothetical prote	246	31	55.4	1043	2	A56037	1-phosphatidylinos
174	31	55.4	197	2	H87491	NADH dehydrogenase	247	31	55.4	1093	2	T18275	cell division prot
175	31	55.4	216	2	H69221	hypothetical prote	248	31	55.4	1343	2	AF0611	cell division prot

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:19:39 ; Search time 18.3333 Seconds
(without alignments)
57.730 Million cell updates/sec

Title: US-10-091-135-10
Perfect score: 56
Sequence: 1 LTGSTAAKYDD 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	204	2 A44583	venom allergen ant
2	51	91.1	204	2 B44583	venom allergen ant
3	45	80.4	204	2 C44583	venom allergen ant
4	44	78.6	204	2 B37329	antigen 5 - easter
5	40	71.4	787	2 D75325	glutamine synthase
6	38	67.9	827	2 T04789	hypothetical prote
7	37	66.1	242	2 C37760	NADH2 dehydrogenas
8	37	66.1	359	2 T42524	hypothetical prote
9	37	66.1	412	2 G47336	yadC protein - Esc
10	37	66.1	476	2 T41619	hypothetical prote
11	37	66.1	744	2 AG1382	transport protein
12	37	66.1	744	2 AD1751	transport protein
13	36	64.3	172	2 S65487	light-harvesting c
14	36	64.3	1361	2 T03415	S-layer protein -
15	36	64.3	1373	1 A33291	collagen alpha 2(I
16	36	64.3	1785	2 T22595	hypothetical prote
17	35	62.5	197	2 E71692	NADH2 dehydrogenas
18	35	62.5	311	1 C63101	conserved hypothet
19	35	62.5	396	2 G82862	conjugal transfer
20	35	62.5	396	2 A87403	translation elonga
21	35	62.5	419	2 A95125	hypothetical prote
22	35	62.5	419	2 E97995	UDP-N-acetylglucos
23	35	62.5	632	2 F36544	hypothetical prote
24	35	62.5	669	2 B36036	probable aldehyde
25	35	62.5	913	2 JCS463	alpha-glucosidase
26	35	62.5	1575	2 S68448	synaptojanin, 170K
27	34	60.7	46	2 D71317	hypothetical prote
28	34	60.7	298	2 T36554	hypothetical prote
29	34	60.7	311	2 A84321	hypothetical prote

30	34	60.7	369	2 C97994	rNA polymerase eig
31	34	60.7	369	2 A95124	rNA polymerase eig
32	34	60.7	385	2 AH2169	ABC transport syst
33	34	60.7	388	1 S22387	cuticle-degrading
34	34	60.7	399	2 F89978	conserved hypothet
35	34	60.7	442	2 A13075	glutamate synthase
36	34	60.7	442	2 H98210	glutamC protein (i
37	34	60.7	466	1 C53402	cysteine-tRNA liga
38	34	60.7	682	1 HHBYK2	dnak-type molecula
39	34	60.7	696	2 B97227	glutamine syntheta
40	34	60.7	788	2 S67595	hypothetical prote
41	34	60.7	902	2 T48531	alpha-glucosidase
42	34	60.7	954	2 A10438	probable exported
43	34	60.7	1188	2 S48861	gene ei protein -
44	34	60.7	2492	1 A44213	nonstructural poly
45	34	60.7	2492	1 C44213	nonstructural poly
46	34	60.7	2492	1 MNWVTD	hypothetical prote
47	33	58.9	112	2 G70855	hypothetical prote
48	33	58.9	125	2 E75624	thioredoxin f prec
49	33	58.9	182	2 T07837	NADH2 dehydrogenas
50	33	58.9	204	2 S78165	ribose 5-phosphate
51	33	58.9	218	2 AD0112	ribose 5-phosphate
52	33	58.9	219	2 AE0874	ribosephosphate is
53	33	58.9	219	2 A98102	ribose 5-phosphate
54	33	58.9	219	2 A65076	ribosephosphate is
55	33	58.9	219	2 E85947	hypothetical prote
56	33	58.9	238	2 H87299	probable membrane
57	33	58.9	239	2 S64324	probable transcrip
58	33	58.9	270	2 C83167	conserved hypothet
59	33	58.9	310	2 E75476	probable integral
60	33	58.9	330	2 T36695	Similar to NU27 l1
61	33	58.9	371	2 F96754	translation elonga
62	33	58.9	410	2 S04391	hypothetical prote
63	33	58.9	412	2 F89905	NAD(FAD)-dependent
64	33	58.9	417	2 A97083	NADH dehydrogenase
65	33	58.9	419	2 D86728	lytic murein trans
66	33	58.9	421	2 AG2587	hypothetical prote
67	33	58.9	421	2 G97369	hypothetical prote
68	33	58.9	531	2 S36537	L1 protein - human
69	33	58.9	714	2 AE1353	penicillin-binding
70	33	58.9	769	2 D86335	T20H2.6 protein -
71	33	58.9	847	2 A48228	beta-N-acetylhexos
72	33	58.9	869	2 S49844	probable membrane
73	33	58.9	1186	2 AD1300	Smc protein essent
74	33	58.9	1355	1 VGBE11	149K glycoprotein
75	33	58.9	1609	2 S44821	F44E2.4 protein -
76	33	58.9	2182	2 T14320	calcineurin inhibi
77	32.5	58.0	454	2 C82682	glutamate-cysteine
78	32	57.1	44	2 B39859	flavocytochrome c
79	32	57.1	73	2 JS0107	hypothetical 7.4K
80	32	57.1	97	1 BVECGS	chaperonin GroES -
81	32	57.1	97	2 C91269	chaperonin GroES [
82	32	57.1	97	2 A86110	chaperonin mopB [a
83	32	57.1	127	2 S49195	GCR 20 protein - f
84	32	57.1	136	2 H85909	partial probable t
85	32	57.1	144	2 H45725	probable transposa
86	32	57.1	149	2 D47169	flavocytochrome c,
87	32	57.1	158	2 T05007	hypothetical prote
88	32	57.1	196	2 D72129	maf protein CP0754
89	32	57.1	196	2 H86493	Mat-type protein [
90	32	57.1	206	2 T44469	transposase tnpC [
91	32	57.1	215	2 A85745	hypothetical prote
92	32	57.1	215	2 D85977	probable transposa
93	32	57.1	215	2 C85695	probable transposa
94	32	57.1	215	2 A85715	hypothetical prote
95	32	57.1	217	2 B90765	hypothetical prote
96	32	57.1	229	2 E85806	hypothetical prote
97	32	57.1	229	2 D90958	NADH-ubiquinone ox
98	32	57.1	250	2 E82821	hypothetical prote
99	32	57.1	250	2 T15415	hypothetical prote
100	32	57.1	288	2 F85818	hypothetical prote
101	32	57.1	290	2 C95012	hypothetical prote
102	32	57.1	290	2 F97883	L-serine ammonia-1

98	33	58.9	69	8	ABO55487	Abos5487 Human gen'	171	32	57.1	19	4	AAU04212	Aau04212 Chaperon
99	33	58.9	123	4	ABG26198	Abg26198 Novel hum	172	32	57.1	56	6	AAU39894	Aau39894 Propionib
100	33	58.9	169	4	AG82185	Ag82185 S. epider	173	32	57.1	56	6	ABM36413	Abm36413 Propionib
101	33	58.9	173	4	ABBS58373	Abbs58373 Drosophil	174	32	57.1	71	4	ADM19978	Adm19978 Protein e
102	33	58.9	178	3	AGB13366	Agb13366 Arabidops	175	32	57.1	97	2	AAE67390	Aae67390 E. coli G
103	33	58.9	178	5	ABP60703	Abp60703 Arabidops	176	32	57.1	97	3	AAV99622	Aav99622 Escherich
104	33	58.9	178	8	ADN74765	Adn74765 Thale cre	177	32	57.1	97	3	AAU34861	Aau34861 E. coli c
105	33	58.9	182	5	ABP60705	Abp60705 Brassica	178	32	57.1	97	8	ADR93337	Adr93337 E. coli p
106	33	58.9	217	5	ABP77514	Abp77514 Borrelia	179	32	57.1	104	6	ABP79837	Abp79837 N. gonorr
107	33	58.9	223	5	ABP26779	Abp26779 Streptoco	180	32	57.1	107	4	ABF79578	Abf79578 Corynebac
108	33	58.9	223	8	ADV89314	Adv89314 Streptoco	181	32	57.1	107	4	ABG33012	Abg33012 C. glutami
109	33	58.9	223	8	ADV80567	Adv80567 Streptoco	182	32	57.1	117	7	ABO62049	AbO62049 Klebsiell
110	33	58.9	223	8	ADV82737	Adv82737 Streptoco	183	32	57.1	117	7	ABG71799	Abg71799 Drosophil
111	33	58.9	226	4	ABB71068	Abb71068 Drosophil	184	32	57.1	127	4	ABX92313	Abx92313 Plant ful
112	33	58.9	226	4	ABBY0364	Abby0364 Drosophil	185	32	57.1	132	5	ABG71272	Abg71272 Human lis
113	33	58.9	242	6	ABU29581	Abu29581 Protein e	186	32	57.1	132	8	ADY23855	Ady23855 Plant ful
114	33	58.9	258	6	ADA332138	Ada332138 Acinetoba	187	32	57.1	142	6	ABR44235	AbR44235 Human sec
115	33	58.9	260	7	ABO85502	AbO85502 Klebsiell	188	32	57.1	154	6	ABU63125	Abu63125 Human gro
116	33	58.9	270	8	ADY23602	Ady23602 Plant ful	189	32	57.1	154	8	ADX75047	Adx75047 Plant ful
117	33	58.9	289	4	AAE65676	Aae65676 Novel pro	190	32	57.1	165	8	ADX75674	Adx75674 Plant ful
118	33	58.9	289	8	ADI29284	Adi29284 Mouse MAR	191	32	57.1	170	8	ADX75212	Adx75212 Plant ful
119	33	58.9	311	8	ADY04710	Ady04710 Plant ful	192	32	57.1	170	8	ADB09602	AdB09602 Alloiococ
120	33	58.9	333	4	AAU44840	Aau44840 Propionib	193	32	57.1	180	6	ABY34621	AbY34621 Chlamydia
121	33	58.9	333	6	ABM41359	Abm41359 Propionib	194	32	57.1	196	2	AAV34621	Aav34621 Novel hum
122	33	58.9	336	7	ABO74151	AbO74151 Pseudomon	195	32	57.1	202	4	ABG24177	AbG24177 Novel hum
123	33	58.9	346	8	ABU33375	Abu33375 Protein e	196	32	57.1	204	6	ABO809604	AbO809604 Alloiococ
124	33	58.9	347	6	ABU33375	Abu33375 Protein e	197	32	57.1	217	7	ADC00401	AdC00401 Enterohae
125	33	58.9	355	6	ABM65336	Abm65336 Propionib	198	32	57.1	218	3	AAAY44507	AaY44507 C-termina
126	33	58.9	371	3	AAU35871	Aau35871 Arabidops	199	32	57.1	218	3	AAAG04640	AaG04640 Arabidops
127	33	58.9	390	4	AAU35090	Aau35090 Enterococ	200	32	57.1	218	3	AAAG050649	AaG050649 Arabidops
128	33	58.9	390	6	ABU29301	Abu29301 Protein e	201	32	57.1	229	9	ADW18653	AdW18653 Pinus rad
129	33	58.9	401	8	ADS24061	Ads24061 Bacterial	202	32	57.1	229	6	ADB07948	AdB07948 Alloiococ
130	33	58.9	412	6	ABM71873	Abm71873 Staphyloc	203	32	57.1	229	3	ADC01133	AdC01133 Enterohae
131	33	58.9	412	6	ABM71873	Abm71873 Staphyloc	204	32	57.1	230	3	AAAG050648	AaG050648 Arabidops
132	33	58.9	417	5	ABP39306	Abp39306 Staphyloc	205	32	57.1	234	8	ADJ49491	AdJ49491 Oil-assoc
133	33	58.9	417	5	ADS04936	Ads04936 Staphyloc	206	32	57.1	235	3	AAAG04639	AaG04639 Arabidops
134	33	58.9	419	5	ABBS4141	Abbs4141 Lactococ	207	32	57.1	235	6	ABU24467	Abu24467 Protein e
135	33	58.9	428	8	ADQ74950	Adq74950 Pseudomon	208	32	57.1	249	8	ABH39783	AbH39783 Streptomy
136	33	58.9	436	4	ABG30368	Abg30368 Novel hum	209	32	57.1	254	7	ABO61274	AbO61274 Klebsiell
137	33	58.9	462	8	ADS24409	Ads24409 Bacterial	210	32	57.1	259	8	ADJ48919	AdJ48919 Oil-assoc
138	33	58.9	469	8	ADN60465	Adn60465 B. lichen	211	32	57.1	271	8	ADJ48919	AdJ48919 Oil-assoc
139	33	58.9	491	4	ABG28562	Abg28562 Novel hum	212	32	57.1	272	4	AG82598	Ag82598 S. epider
140	33	58.9	517	9	ABM91917	Abm91917 M. xanthu	213	32	57.1	285	6	ADA36196	Ada36196 Acinetoba
141	33	58.9	520	4	AAH80105	Aah80105 Corynebac	214	32	57.1	290	6	ABU00436	Abu00436 S. pneumo
142	33	58.9	520	4	AAH80105	Aah80105 Corynebac	215	32	57.1	290	8	ADK48468	AdK48468 Streptoco
143	33	58.9	608	7	ABM86676	Abm86676 Rice abio	216	32	57.1	294	9	AEA59560	Aea59560 Streptoco
144	33	58.9	693	8	ADK68676	Adk68676 Rhizobium	217	32	57.1	295	4	ABBS2831	Abbs2831 Escherich
145	33	58.9	702	8	ADN21371	Adn21371 Bacterial	218	32	57.1	295	7	ADC00169	AdC00169 Enterohae
146	33	58.9	714	5	ABBA49056	Abba49056 Listeria	219	32	57.1	295	7	ADC01600	AdC01600 Enterohae
147	33	58.9	730	3	AAU72892	Aau72892 Human met	220	32	57.1	296	4	ABBS2580	Abbs2580 Escherich
148	33	58.9	731	5	AAU72892	Aau72892 Arabidops	221	32	57.1	296	4	ABBS2746	Abbs2746 Escherich
149	33	58.9	748	3	AAU72892	Aau72892 Arabidops	222	32	57.1	296	7	ADC01609	AdC01609 Enterohae
150	33	58.9	748	5	ABBS91075	Abbs91075 Herbicida	223	32	57.1	296	7	ADC01596	AdC01596 Enterohae
151	33	58.9	769	3	AAU72892	Aau72892 Arabidops	224	32	57.1	296	7	ADC01307	AdC01307 Enterohae
152	33	58.9	837	4	ABBS58272	Abbs58272 Drosophil	225	32	57.1	296	7	ADC00248	AdC00248 Enterohae
153	33	58.9	847	2	AAW85603	Aaw85603 Hexosamin	226	32	57.1	296	7	ADC01104	AdC01104 Enterohae
154	33	58.9	851	4	AAU72617	Aau72617 Carassius	227	32	57.1	296	7	ADC00530	AdC00530 Enterohae
155	33	58.9	1028	7	ABM88667	Abm88667 Rice abio	228	32	57.1	296	7	ADC00742	AdC00742 Enterohae
156	33	58.9	1085	6	ABU31244	Abu31244 Protein e	229	32	57.1	296	7	ADC01593	AdC01593 Enterohae
157	33	58.9	1085	6	ABU28426	Abu28426 Protein e	230	32	57.1	296	7	ADC00742	AdC00742 Enterohae
158	33	58.9	1121	6	ADA26484	Ada26484 Alpha-iso	231	32	57.1	296	7	ADC00530	AdC00530 Enterohae
159	33	58.9	1186	5	ABBA48890	Abba48890 Listeria	232	32	57.1	296	7	ADC00022	AdC00022 Enterohae
160	33	58.9	1186	6	ABU32422	Abu32422 Protein e	233	32	57.1	296	7	ADC00643	AdC00643 Enterohae
161	33	58.9	1356	8	ADS30542	Ads30542 Bacterial	234	32	57.1	296	7	ADC01268	AdC01268 Enterohae
162	33	58.9	1627	7	ADA35317	Ada35317 Acinetoba	235	32	57.1	296	7	ADC01602	AdC01602 Enterohae
163	33	58.9	2182	7	ADE55128	Ade55128 Rat Prote	236	32	57.1	299	8	ADU02483	AdU02483 Novel hum
164	33	58.9	2182	7	ADE55124	Ade55124 Rat Prote	237	32	57.1	309	9	AAAY3770	AaY3770 Chlamydia
165	33	58.9	2272	4	ABBB70004	Abb70004 Drosophil	238	32	57.1	323	2	AAAY3770	AaY3770 Chlamydia
166	33	58.9	2272	4	ABBB70004	Abb70004 Drosophil	239	32	57.1	323	9	ABE25209	AbE25209 IHNV env
167	32.5	58.0	343	3	ABP64772	Abp64772 Human sec	240	32	57.1	333	5	ADII17211	AdI17211 Cat NOVX
168	32.5	58.0	343	6	ABR01118	AbR01118 Human gen	241	32	57.1	333	5	ADII17211	AdI17211 Cat NOVX
169	32.5	58.0	343	7	ADC20431	AdC20431 Human sec	242	32	57.1	333	5	ADII17211	AdI17211 Cat NOVX
170	32.5	58.0	436	6	ABU11851	Abu11851 Human sec	243	32	57.1	333	7	ABM90428	Abm90428 Rice abio

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:13:51 ; Search time 96.7083 Seconds

(without alignments)
49.977 Million cell updates/sec

Title: US-10-091-135-10

Perfect score: 56

Sequence: 1 LTGSTAAKYDD 11

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : A Geneseq 21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	56	100.0	11	5	Aae28816 Vespula v
2	56	100.0	48	5	Aae28813 Vespula v
3	56	100.0	204	2	Aaw35688 Vespida an
4	56	100.0	204	2	Aay45217 Wild type
5	56	100.0	204	5	Abg66977 Wasp veno
6	56	100.0	204	5	Abg66983 Wasp veno
7	56	100.0	204	5	Abg67052 Wasp veno
8	56	100.0	204	5	Abg67104 Wasp veno
9	56	100.0	204	5	Abg67103 Wasp veno
10	56	100.0	204	5	Aae28820 Vespula v
11	56	100.0	209	4	Abm00031 Allergen
12	56	100.0	227	2	Aay25644 Vespula s
13	56	100.0	227	4	Aae13071 Vespula v
14	56	100.0	227	4	Adc34893 Wasp alle
15	44	78.6	204	2	Aaw35687 Vespida an
16	40	71.4	214	4	Abg23626 Novel hum
17	37	66.1	18	8	Adl93350 Anti-V5 a
18	37	66.1	171	4	Abg12148 Novel hum
19	37	66.1	412	4	Aag98283 Escherich
20	37	66.1	412	6	Abu14812 Protein e
21	37	66.1	744	5	Abb49954 Listeria
22	37	66.1	1136	5	Adj33677 Protein o
23	37	66.1	1137	4	Abg28828 Novel hum
24	37	66.1	5183	8	Ado44006 Amino aci

25	37	66.1	5183	9	ADx06154	Cyclin-de
26	36	64.3	315	8	ADT58851	Plant pol
27	36	64.3	587	7	ADL15066	Human adu
28	36	64.3	1372	7	ADe59683	Rat Prote
29	36	64.3	1372	7	ADd45148	Rat Prote
30	36	64.3	1372	7	ADd45604	Rat Prote
31	36	64.3	1372	7	ADe59687	Rat Prote
32	36	64.3	1372	7	ADd47529	Rat Prote
33	36	64.3	1373	5	ABb57364	Mouse isc
34	36	64.3	1373	9	ADW44460	Murine pr
35	36	64.3	1785	8	ADn24366	Bacterial
36	35	62.5	91	8	ADx75924	Plant ful
37	35	62.5	133	7	ABM73617	DNA clone
38	35	62.5	178	8	ADx89247	Plant ful
39	35	62.5	179	8	ADx89449	Plant ful
40	35	62.5	200	8	ADY23598	Plant ful
41	35	62.5	251	7	ADc95024	B. faeciu
42	35	62.5	410	4	AAU45865	Propionib
43	35	62.5	410	6	ABM42384	Propionib
44	35	62.5	419	2	AAW80613	S. pneumo
45	35	62.5	419	3	AAy91116	Streptoco
46	35	62.5	419	4	AAU37737	Streptoco
47	35	62.5	419	4	AAU01044	CFE 47 pr
48	35	62.5	419	5	AAU01497	S. pneumo
49	35	62.5	419	6	ABU01497	S. pneumo
50	35	62.5	419	6	ABU46035	Protein e
51	35	62.5	419	8	ADK47251	Streptoco
52	35	62.5	422	8	ADK47251	Streptoco
53	35	62.5	422	9	AEA60058	Novel S.
54	35	62.5	486	4	ABB68533	Streptoco
55	35	62.5	528	6	ABU23082	Drosophil
56	35	62.5	914	6	ABU63150	Wild-type
57	35	62.5	1574	7	ADe55582	Protein e
58	35	62.5	2096	4	ABB65242	Rat Prote
59	35	62.5	2096	8	ADQ89606	Drosophil
60	34	60.7	19	9	ADZ69708	Antagonis
61	34	60.7	159	2	AAy11201	Murine me
62	34	60.7	159	9	ABE41846	S. pneumo
63	34	60.7	171	9	ABE38607	L. pneumo
64	34	60.7	174	5	ABP66316	Bifidobac
65	34	60.7	304	8	ADK47242	Streptoco
66	34	60.7	329	8	ADR95740	Novel S.
67	34	60.7	329	9	AEA59610	Streptoco
68	34	60.7	369	6	ABU01488	S. pneumo
69	34	60.7	369	6	ABU46032	Protein e
70	34	60.7	369	8	ADH97012	S. pneumo
71	34	60.7	369	8	ADH97014	S. pneumo
72	34	60.7	369	9	ABE13367	Streptoco
73	34	60.7	369	9	ABE13369	Streptoco
74	34	60.7	388	2	AAy42435	Cuticle-d
75	34	60.7	401	6	ABM71468	Staphyloc
76	34	60.7	401	9	ABE40964	L. pneumo
77	34	60.7	423	9	ABE37653	L. pneumo
78	34	60.7	468	8	ADN25675	Bacterial
79	34	60.7	682	4	AAg70749	S. cerevis
80	34	60.7	682	6	ABR52837	Protein e
81	34	60.7	682	7	ADK62272	Disease t
82	34	60.7	682	8	ADK62272	Disease t
83	34	60.7	696	8	ADs43737	Bacterial
84	34	60.7	788	6	ABU24188	Protein e
85	34	60.7	788	6	ABR53137	Protein e
86	34	60.7	788	8	ADT87236	Disease t
87	34	60.7	831	6	ABP78978	Yeast Str
88	34	60.7	902	6	ABU63302	N. gonorr
89	34	60.7	927	6	ABU41568	Wild-type
90	34	60.7	954	6	ABU50458	Protein e
91	34	60.7	1060	4	ABB68109	Protein e
92	34	60.7	1169	4	ABB63860	Drosophil
93	34	60.7	1169	4	ABB63867	Drosophil
94	34	60.7	1169	7	ADK11389	Drosophil
95	34	60.7	1169	7	ADK11387	Drosophil
96	34	60.7	2492	5	AAE18302	Venezuela
97	34	60.7	2492	9	ADY26147	Venezuela

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:28:47 ; Search time 10.0833 Seconds
(without alignments)
46.352 Million cell updates/sec

Title: US-10-091-135-9
Perfect score: 60
Sequence: 1 LKPNGKNVVV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Published Applications AA New:
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2: /SIDSS/prodata/2/pubpaa/US06_NEW_PUB.pep:
3: /SIDSS/prodata/2/pubpaa/US07_NEW_PUB.pep:
4: /SIDSS/prodata/2/pubpaa/PCR_NEW_PUB.pep:
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7: /SIDSS/prodata/2/pubpaa/US11_NEW_PUB.pep:
8: /SIDSS/prodata/2/pubpaa/US60_NEW_PUB.pep:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	40	66.7	206	6	US-10-498-026-80
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4	40	66.7	1239	7	US-11-079-463-9073
5	39	65.0	827	6	US-11-226-869-577
6	37	61.7	445	7	US-11-226-869-473
7	37	61.7	466	7	US-11-226-869-472
8	37	61.7	650	7	US-11-226-869-469
9	37	61.7	661	7	US-11-226-869-552
10	37	61.7	743	7	US-11-226-869-494
11	37	61.7	1002	7	US-11-226-869-475
12	37	61.7	1013	7	US-11-226-869-553
13	37	61.7	1095	7	US-11-226-869-493
14	37	61.7	1294	7	US-11-079-463-7324
15	37	61.7	1341	7	US-11-226-869-565
16	37	61.7	1349	7	US-11-226-869-573
17	36	60.0	125	6	US-10-213-535-9
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23	36	60.0	336	6	US-10-793-626-1858
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47	34	56.7	750	6	US-10-195-888-104	Sequence 104, App
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51	34	56.7	750	7	US-11-202-516-2	Sequence 2, Appli
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63	33	55.0	464	7	US-11-087-099-7754	Sequence 6373, Ap
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69	33	55.0	708	6	US-10-821-234-917	Sequence 125, App
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71	33	55.0	790	6	US-10-131-826A-204	Sequence 1138, Ap
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78	32.5	54.2	453	7	US-11-137-465-45	Sequence 44, Appl
79	32	53.3	118	6	US-10-506-454-748	Sequence 748, App
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88	32	53.3	313	7	US-11-052-554A-247	Sequence 247, App
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153	37	61.7	1341	4	US-10-058-270A-4	Sequence 4, Appl	226	36	60.0	125	4	US-10-219-474-94	Sequence 94, Appl
154	37	61.7	1341	5	US-10-855-588-34	Sequence 34, Appl	227	36	60.0	125	4	US-10-219-474-94	Sequence 94, Appl
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172	36	60.0	125	4	US-10-033-245-9	Sequence 9, Appl	245	36	60.0	125	4	US-10-219-474-94	Sequence 94, Appl
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OM protein - protein search, using sw model

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Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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10	60	100.0	203	4	US-10-001-245-118
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89	37	61.7	183	4	US-10-425-115-197149	Sequence 197149,
90	37	61.7	185	4	US-10-767-701-40272	Sequence 40272, A
91	37	61.7	241	4	US-10-133-757-5	Sequence 5, Appli
92	37	61.7	297	5	US-10-732-923-9301	Sequence 9301, Ap
93	37	61.7	343	4	US-10-425-114-41194	Sequence 41194, A
94	37	61.7	382	4	US-10-425-115-255037	Sequence 255037,
95	37	61.7	390	4	US-10-369-493-10319	Sequence 10319, A
96	37	61.7	394	4	US-10-032-585-7381	Sequence 7381, Ap
97	37	61.7	445	3	US-09-835-301-29	Sequence 29, Appli
98	37	61.7	445	3	US-09-604-287A-473	Sequence 473, App
99	37	61.7	445	3	US-09-834-759-473	Sequence 473, App
100	37	61.7	445	3	US-09-551-621-473	Sequence 473, App

101	34	56.7	84	2	US-09-489-039A-7591	Sequence 7591, Ap	174	33	55.0	382	2	US-09-906-700-137	Sequence 137, App
102	34	56.7	84	2	US-09-248-796A-18553	Sequence 18553, A	175	33	55.0	382	2	US-09-903-603A-137	Sequence 137, App
103	34	56.7	84	4	PCT-US93-09523-3	Sequence 3, Appli	176	33	55.0	382	2	US-09-904-920A-137	Sequence 137, App
104	34	56.7	132	2	US-09-589-892B-13	Sequence 13, Appl	177	33	55.0	382	2	US-09-909-064-137	Sequence 137, App
105	34	56.7	147	2	US-09-270-767-34148	Sequence 34148, A	178	33	55.0	382	2	US-09-905-381A-137	Sequence 137, App
106	34	56.7	147	2	US-09-270-767-49355	Sequence 49355, A	179	33	55.0	382	2	US-09-906-618-137	Sequence 137, App
107	34	56.7	196	2	US-09-540-326-3127	Sequence 3127, Ap	180	33	55.0	382	2	US-09-906-646-137	Sequence 137, App
108	34	56.7	210	1	US-09-320-559-4	Sequence 4, Appli	181	33	55.0	382	2	US-09-904-462-137	Sequence 137, App
109	34	56.7	210	1	US-09-327-392-4	Sequence 4, Appli	182	33	55.0	382	2	US-09-906-722A-137	Sequence 137, App
110	34	56.7	210	1	US-08-545-860D-4	Sequence 4, Appli	183	33	55.0	382	2	US-09-906-722A-137	Sequence 137, App
111	34	56.7	210	4	PCT-US94-04496-4	Sequence 4, Appli	184	33	55.0	384	2	US-09-248-796A-18132	Sequence 18132, A
112	34	56.7	220	2	US-09-004-731-95	Sequence 95, Appl	185	33	55.0	425	2	US-09-252-991A-20831	Sequence 20831, A
113	34	56.7	220	2	US-08-749-699-95	Sequence 95, Appl	186	33	55.0	474	2	US-09-774-639-371	Sequence 371, App
114	34	56.7	220	2	US-09-004-729-95	Sequence 95, Appl	187	33	55.0	500	2	US-09-538-092-831	Sequence 831, App
115	34	56.7	226	2	US-09-004-731-8	Sequence 8, Appli	188	33	55.0	521	2	US-09-221-294-2	Sequence 2, Appli
116	34	56.7	226	2	US-08-749-699-8	Sequence 8, Appli	189	33	55.0	563	2	US-09-902-540-9999	Sequence 9999, Ap
117	34	56.7	226	2	US-09-004-729-8	Sequence 8, Appli	190	33	55.0	568	2	US-09-902-540-9999	Sequence 9999, Ap
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119	34	56.7	254	2	US-09-004-731-92	Sequence 92, Appl	192	33	55.0	631	2	US-08-448-489-17	Sequence 17, Appl
120	34	56.7	254	2	US-08-749-699-89	Sequence 89, Appl	193	33	55.0	660	2	US-09-689-730-17	Sequence 17, Appl
121	34	56.7	254	2	US-08-749-699-92	Sequence 92, Appl	194	33	55.0	660	2	US-08-704-711A-18	Sequence 18, Appl
122	34	56.7	254	2	US-09-004-729-89	Sequence 89, Appl	195	33	55.0	660	2	US-09-521-220-18	Sequence 18, Appl
123	34	56.7	254	2	US-09-004-729-92	Sequence 92, Appl	196	33	55.0	660	2	US-09-391-104-19	Sequence 19, Appl
124	34	56.7	327	2	US-09-004-731-2	Sequence 2, Appli	197	33	55.0	660	2	US-09-917-254-89	Sequence 89, Appl
125	34	56.7	327	2	US-09-004-731-5	Sequence 5, Appli	198	33	55.0	660	2	US-09-949-016-7937	Sequence 6512, Ap
126	34	56.7	327	2	US-08-749-699-2	Sequence 2, Appli	199	33	55.0	660	2	US-09-949-016-7937	Sequence 7937, Ap
127	34	56.7	327	2	US-08-749-699-5	Sequence 5, Appli	200	33	55.0	660	2	US-10-153-185-14	Sequence 14, Appl
128	34	56.7	327	2	US-09-004-729-2	Sequence 2, Appli	201	33	55.0	663	2	US-09-194-468A-30	Sequence 30, Appl
129	34	56.7	327	2	US-09-004-729-5	Sequence 5, Appli	202	33	55.0	674	2	US-09-270-767-43706	Sequence 43706, A
130	34	56.7	368	2	US-09-270-767-61640	Sequence 61640, A	203	33	55.0	752	2	US-09-910-039-235	Sequence 235, App
131	34	56.7	468	2	US-09-710-279-1648	Sequence 1428, Ap	204	33	55.0	752	2	US-09-910-039-235	Sequence 235, App
132	34	56.7	471	2	US-09-134-001C-4125	Sequence 4125, Ap	205	33	55.0	778	2	US-09-134-001C-4023	Sequence 4023, Ap
133	34	56.7	480	2	US-09-965-902A-2	Sequence 4, Appli	206	33	55.0	781	2	US-09-248-796A-18066	Sequence 18066, A
134	34	56.7	493	2	US-09-270-767-46087	Sequence 46087, A	207	33	55.0	781	2	US-09-949-016-6959	Sequence 6959, Ap
135	34	56.7	552	2	US-09-120-365-5	Sequence 5, Appli	208	33	55.0	790	2	US-09-949-016-7017	Sequence 7017, Ap
136	34	56.7	552	2	US-09-515-039-5	Sequence 5, Appli	209	33	55.0	790	2	US-09-949-016-8169	Sequence 8169, Ap
137	34	56.7	569	2	US-10-104-047-3373	Sequence 3373, Ap	210	33	55.0	790	2	US-09-949-016-8170	Sequence 8170, Ap
138	34	56.7	616	2	US-08-965-902A-2	Sequence 2, Appli	211	33	55.0	852	1	US-09-070-060-3	Sequence 3, Appli
139	34	56.7	693	2	US-08-705-477E-101	Sequence 101, App	212	33	55.0	852	1	US-09-357-746-3	Sequence 3, Appli
140	34	56.7	700	2	US-09-107-532A-5094	Sequence 5094, Ap	213	33	55.0	854	1	US-09-070-060-4	Sequence 4, Appli
141	34	56.7	707	1	US-09-528-122-18	Sequence 18, Appl	214	33	55.0	854	1	US-09-357-746-4	Sequence 4, Appli
142	34	56.7	707	1	PCT-US95-11720-18	Sequence 18, Appl	215	33	55.0	1239	1	US-08-937-931-2	Sequence 2, Appli
143	34	56.7	737	2	US-09-583-110-4156	Sequence 4156, Ap	216	33	55.0	1239	2	US-09-285-502-2	Sequence 2, Appli
144	34	56.7	750	1	US-08-325-553-2	Sequence 2, Appli	217	33	55.0	1239	2	US-09-709-126-2	Sequence 2, Appli
145	34	56.7	750	1	US-09-394-152A-2	Sequence 2, Appli	218	33	55.0	1239	2	US-09-871-385A-2	Sequence 2, Appli
146	34	56.7	750	1	US-09-044-668-2	Sequence 2, Appli	219	33	55.0	1362	2	US-09-134-001C-4955	Sequence 4955, Ap
147	34	56.7	750	2	US-09-705-477E-2	Sequence 2, Appli	220	33	55.0	1442	2	US-09-320-095-2	Sequence 2052, Ap
148	34	56.7	750	2	US-09-972-382C-4	Sequence 4, Appli	221	32	54.2	62	2	US-09-320-095-2	Sequence 2, Appli
149	34	56.7	750	2	US-09-999-833A-618	Sequence 618, App	222	32	54.2	62	2	US-09-320-095-10	Sequence 10, Appl
150	34	56.7	750	2	US-08-466-381C-2	Sequence 2, Appli	223	32	54.2	557	2	US-09-523-487-2	Sequence 10, Appl
151	34	56.7	750	2	US-10-020-445A-618	Sequence 618, App	224	32	54.2	557	2	US-09-523-487-10	Sequence 60, Appl
152	34	56.7	750	2	US-09-561-502-2	Sequence 2, Appli	225	32	53.3	43	1	US-08-488-161-60	Sequence 60, Appl
153	34	56.7	751	2	US-09-107-433-4728	Sequence 4728, Ap	226	32	53.3	43	2	US-09-273-685-60	Sequence 60, Appl
154	34	56.7	769	2	US-09-320-878-12	Sequence 12, Appl	227	32	53.3	43	4	PCT-US95-11934-60	Sequence 60, Appl
155	34	56.7	769	2	US-09-141-908-10	Sequence 10, Appl	228	32	53.3	65	2	US-09-107-532A-6494	Sequence 6494, Ap
156	34	56.7	769	2	US-09-657-440-12	Sequence 12, Appl	229	32	53.3	130	2	US-09-248-796A-19515	Sequence 19515, A
157	34	56.7	769	2	US-09-783-708-12	Sequence 12, Appl	230	32	53.3	179	2	US-09-605-703B-2850	Sequence 2850, Ap
158	34	56.7	774	2	US-09-902-540-9843	Sequence 9843, Ap	231	32	53.3	189	2	US-09-800-729-144	Sequence 144, App
159	34	56.7	784	2	US-09-740-235-1	Sequence 1, Appli	232	32	53.3	212	2	US-09-270-767-42473	Sequence 42473, A
160	34	56.7	809	2	US-09-105-537-24	Sequence 24, Appl	233	32	53.3	223	2	US-09-949-016-8894	Sequence 8894, Ap
161	34	56.7	1048	2	US-09-171-699-10	Sequence 10, Appl	234	32	53.3	267	2	US-09-519-232-68	Sequence 68, Appl
162	34	56.7	1165	2	US-09-902-540-12897	Sequence 12897, A	235	32	53.3	282	2	US-09-252-991A-28272	Sequence 28272, A
163	34	56.7	3782	2	US-09-105-537-4	Sequence 4, Appli	236	32	53.3	313	2	US-09-303-518D-314	Sequence 314, App
164	33	55.0	43	2	US-10-153-185-15	Sequence 15, Appl	237	32	53.3	313	2	US-08-225-477B-316	Sequence 316, App
165	33	55.0	44	2	US-10-153-185-2	Sequence 2, Appli	238	32	53.3	329	1	US-08-225-477B-316	Sequence 3, Appli
166	33	55.0	61	2	US-09-107-532A-5570	Sequence 5570, Ap	239	32	53.3	329	1	PCT-US95-04353-3	Sequence 8, Appli
167	33	55.0	73	2	US-09-248-796A-22754	Sequence 22754, A	240	32	53.3	334	2	US-08-379-556A-8	Sequence 13658, A
168	33	55.0	260	2	US-09-638-203-3	Sequence 3, Appli	241	32	53.3	337	2	US-09-434-613-1	Sequence 1, Appli
169	33	55.0	275	2	US-09-468-433C-24	Sequence 24, Appl	242	32	53.3	337	2	US-09-963-908-1	Sequence 1, Appli
170	33	55.0	374	2	US-09-489-847-166	Sequence 166, App	243	32	53.3	337	2	US-10-847-165-1	Sequence 1, Appli
171	33	55.0	382	2	US-09-907-794A-137	Sequence 137, App	244	32	53.3	337	2	US-10-847-165-1	Sequence 6, Appli
172	33	55.0	382	2	US-09-905-125A-137	Sequence 137, App	245	32	53.3	486	2	US-09-716-865-6	Sequence 16, Appl
173	33	55.0	382	2	US-09-902-775A-137	Sequence 137, App	246	32	53.3	492	2	US-09-519-232-16	Sequence 16, Appl

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:24:04 ; Search time 15.3542 Seconds
(without alignments)
59.230 Million cell updates/sec

Title: US-10-091-135-9
Perfect score: 60
Sequence: 1 LKPCGNKVVV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents AA:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	204	1	US-08-419-414-9
2	60	100.0	204	1	US-08-614-935-2
3	60	100.0	204	2	US-09-130-287-2
4	60	100.0	227	2	US-09-541-759-6
5	56	93.3	31	1	US-08-614-935-46
6	56	93.3	31	2	US-09-130-287-46
7	54	90.0	204	1	US-08-614-935-1
8	54	90.0	204	2	US-09-130-287-1
9	50	83.3	31	1	US-08-614-935-45
10	50	83.3	31	2	US-09-130-287-45
11	48	80.0	32	1	US-08-614-935-48
12	48	80.0	32	2	US-09-130-287-48
13	48	80.0	205	1	US-08-614-935-4
14	48	80.0	205	2	US-09-130-287-4
15	47	78.3	31	1	US-08-614-935-47
16	47	78.3	31	2	US-09-130-287-47
17	47	78.3	203	1	US-08-419-414-8
18	47	78.3	203	1	US-08-614-935-3
19	47	78.3	203	2	US-09-130-287-3
20	43	71.7	20	1	US-08-614-935-10
21	43	71.7	20	2	US-09-130-287-10
22	43	71.7	32	1	US-08-614-935-49
23	43	71.7	32	2	US-09-130-287-49
24	43	71.7	204	1	US-08-614-935-5
25	43	71.7	204	2	US-09-130-287-5
26	40	66.7	1011	2	US-09-602-362E-27
27	40	66.7	1239	2	US-10-076-622-577

105	37	61.7	394	2	Q5APB4 CANAL	Q5apb4 candida alb	178	36	60.0	402	2	Q9AL21_ENTFCA	Q9al21 enterococcus
106	37	61.7	406	2	Q9L602_MYCAV	Q9l602 mycobacteri	179	36	60.0	437	2	Q871h0_NEUCR	Q871h0 neurospora
107	37	61.7	414	2	Q6LQ07_PHOPR	Q6lq07 photobacter	180	36	60.0	438	2	Q61ha9_DROME	Q61ha9 drosophila
108	37	61.7	434	2	Q5YA97_9CAUD	Q5ya97 bacillus cl	181	36	60.0	441	2	Q4HX18_GIBZE	Q4hx18 gibberella
109	37	61.7	589	2	Q4L9X3_STAHI	Q4l9x3 staphylococ	182	36	60.0	448	2	Q5B4X6_EMENI	Q5b4x6 aspergillus
110	37	61.7	613	2	Q8TPP0_METAC	Q8tp0 methanosarc	183	36	60.0	459	2	Q45984_CAEEL	Q45984 caenorhabdi
111	37	61.7	623	2	Q83ZD7_STAUA	Q83zd7 staphylococ	184	36	60.0	462	2	Q51N60_MAGGR	Q51n60 magnaporthe
112	37	61.7	641	2	Q5IRN0_MOUSE	Q5irn0 mus musculu	185	36	60.0	479	2	Q7NVB1_CHRVO	Q7nvb1 chromobacte
113	37	61.7	653	2	Q8K100_MOUSE	Q8k100 mus musculu	186	36	60.0	481	2	Q7S7L7_NEUCR	Q7s7l7 neurospora
114	37	61.7	653	2	Q8K100_MOUSE	Q8k100 mus musculu	187	36	60.0	494	2	Q4WNT9_ASFPU	Q4wnt9 aspergillus
115	37	61.7	681	2	Q7Q104_ANOGA	Q7q104 anopheles g	188	36	60.0	545	2	Q4UHV6_THEAB	Q4uhv6 thelleria a
116	37	61.7	692	2	Q5US47_9LECA	Q5us47 sarcogyne s	189	36	60.0	571	2	Q97DE4_CLOAB	Q97de4 clostridium
117	37	61.7	704	2	Q6YK77_TOXGO	Q6yk77 toxoplasma	190	36	60.0	576	2	Q92EN3_SYNV3	Q92en3 synochocyt
118	37	61.7	710	2	Q9FNC7_ARATH	Q9fnc7 arabidopsis	191	36	60.0	644	2	Q92EN3_SYNV3	Q92en3 listeria in
119	37	61.7	711	2	Q5US93_9LECA	Q5us93 acarospora	192	36	60.0	653	2	Q41AP6_GIBZE	Q41ap6 gibberella
120	37	61.7	717	2	Q94114_ARATH	Q94114 arabidopsis	193	36	60.0	707	2	Q5ZJH4_CHICK	Q5zjh4 gallus gall
121	37	61.7	741	2	Q6K9F7_ORYSA	Q6k9f7 oryza sativ	194	36	60.0	714	2	Q60149_STRPY	Q60149 streptococ
122	37	61.7	829	2	SIP4_YEAST	P46954 saccharomyc	195	36	60.0	717	2	Q6PST6_SPOPR	Q6pst6 spodoptera
123	37	61.7	968	2	Q7PST6_ANOGA	Q7psv6 anopheles g	196	36	60.0	806	2	Q9VFV0_DROME	Q9vfv0 drosophila
124	37	61.7	1128	2	Q7TSL2_GVCL	Q7tsl2 cryptophleb	197	36	60.0	842	2	Q97DB8_CLOAB	Q97db8 clostridium
125	37	61.7	1131	2	Q91EW5_GVCP	Q91ew5 cydia pomon	198	36	60.0	850	2	Q54R85_DICDI	Q54r85 dictyosteli
126	37	61.7	1234	2	Q64R22_BACPR	Q64r22 bacteroides	199	36	60.0	850	2	Q60182_SCHZOACCH	Q60182 schizosacch
127	37	61.7	1249	2	Q5LAW4_BACFN	Q5law4 bacteroides	200	36	60.0	934	1	Q61419_STRPY	Q61419 streptococ
128	37	61.7	1341	2	Q5W025_HUMAN	Q5w025 homo sapien	201	36	60.0	981	2	Q62021_ORYSA	Q62021 oryza sativ
129	37	61.7	1341	2	Q9BXX3_HUMAN	Q9bxx3 homo sapien	202	36	60.0	1048	1	Q62021_ORYSA	Q62021 oryza sativ
130	37	61.7	1460	2	Q5W026_HUMAN	Q5w026 homo sapien	203	36	60.0	1234	2	Q8A6Z2_BACTN	Q8a6z2 bacteroides
131	37	61.7	1882	2	Q857A5_9CAUD	Q857a5 mycobacteri	204	36	60.0	1285	2	Q752A3_ASHGO	Q752a3 ashaya goes
132	37	61.7	3843	2	Q9U5D0_DROME	Q9u5d0 drosophila	205	36	60.0	1306	2	Q5NCK4_MOUSE	Q5nck4 mus musculu
133	37	61.7	3843	2	Q9U5D0_DROME	Q9u5d0 drosophila	206	36	60.0	1390	2	Q51UE4_MAGGR	Q51ue4 magnaporthe
134	36	60.0	66	1	RS27_SULSO	Q9v934 drosophila	207	36	60.0	1422	2	Q692A2_MOUSE	Q692a2 mus musculu
135	36	60.0	73	1	RS27_AERPE	Q97z80 sulfolobus	208	36	60.0	1514	2	Q9H0B0_HUMAN	Q9h0b0 homo sapien
136	36	60.0	82	2	Q5BS94_SCHJA	Q5bf01 aeropyrum p	209	36	60.0	1563	2	Q5NCK5_MOUSE	Q5nck5 mus musculu
137	36	60.0	92	2	Q69JEB_ORYSA	Q6bs94 schistosoma	210	36	60.0	1564	2	Q96JN8_HUMAN	Q96jn8 homo sapien
138	36	60.0	96	2	Q92TJ4_MAIZE	Q69jeb oryza sativ	211	36	60.0	1792	2	Q4Z244_PLABE	Q4z244 plasmodium
139	36	60.0	100	2	Q73OM9_TREDE	Q92tj4 zea mays (m	212	35	58.3	55	2	Q8XP03_CLOPE	Q8xp03 clostrid
140	36	60.0	106	2	Q8CR22_STAEP	Q50t97 entamoeba d	213	35	58.3	58	2	Q56BP3_9CAUD	Q56bp3 enterobacte
141	36	60.0	120	2	Q6WLR4_LEGPN	Q6wlr4 legionella	214	35	58.3	70	2	Q6B671_9HIV1	Q6b671 human immun
142	36	60.0	120	2	Q5L5Y4_ENTHI	Q6wlv3 legionella	215	35	58.3	71	2	Q84F10_CLOPE	Q84f10 clostridium
143	36	60.0	122	2	Q515Y4_ENTHI	Q515y4 entamoeba h	216	35	58.3	72	2	Q46251_CLOPE	Q46251 clostridium
144	36	60.0	125	2	Q6UXB1_HUMAN	Q6uxb1 homo sapien	217	35	58.3	76	2	Q95P92_MESMA	Q95p92 mesobuthus
145	36	60.0	171	2	Q50T97_ENTHI	Q50t97 entamoeba h	218	35	58.3	82	2	Q8XQR3_RALSO	Q8xqr3 ralatonia s
146	36	60.0	180	1	S3DR_CLOAB	Q50t97 entamoeba h	219	35	58.3	89	2	Q5PEW8_SALPA	Q5pew8 salmonella
147	36	60.0	180	2	Q6MMK8_BACCE	Q87j95 clostridium	220	35	58.3	90	2	Q5WYF7_LEGPL	Q5wyf7 legionella
148	36	60.0	180	2	Q6HF45_BACHK	Q8mmk8 bacillus ce	221	35	58.3	91	2	Q6K6H2_ORYSA	Q6k6h2 oryza sativ
149	36	60.0	180	2	Q732V6_BACCL	Q6hf45 bacillus th	222	35	58.3	98	2	Q5X705_LEGPA	Q5x705 legionella
150	36	60.0	180	2	Q81A24_BACCR	Q732v6 bacillus ce	223	35	58.3	105	2	Q58622_PYROCCCH	Q58622 pyrococcus
151	36	60.0	180	2	Q63606_BACC2	Q81a24 bacillus ce	224	35	58.3	109	1	Q58622_PYROCCCH	Q58622 pyrococcus
152	36	60.0	180	2	Q63606_BACC2	Q63606 bacillus ce	225	35	58.3	115	2	Q8XZB8_RALSO	Q8xbz8 ralatonia s
153	36	60.0	189	2	Q81WR2_BACAN	Q81wr2 bacillus an	226	35	58.3	118	2	Q15902_TOXGO	Q15902 toxoplasma
154	36	60.0	192	2	Q4L9F5_STAHI	Q87kd9 vibrio para	227	35	58.3	126	2	Q4YZ80_PLABE	Q4yz80 plasmodium
155	36	60.0	214	2	Q624G4_CAEER	Q4l9f5 staphylococ	228	35	58.3	129	1	Y2370_ARCFU	Y2370 archaeoglob
156	36	60.0	221	2	Q6APG7_DESPS	Q624g4 caenorhabdi	229	35	58.3	151	2	Q8LNC2_ORYSA	Q8lnc2 oryza sativ
157	36	60.0	235	2	Q5ZS37_LEGPH	Q6apg7 desulfotale	230	35	58.3	152	2	Q6K7S5_ORYSA	Q6k7s5 oryza sativ
158	36	60.0	238	2	Q4P2V8_USTMA	Q5zs37 legionella	231	35	58.3	162	2	Q96VN5_SULTO	Q96vn5 sulfolobus
159	36	60.0	244	2	Q49533_ARATH	Q4p2v8 ustilago ma	232	35	58.3	163	2	Q77P34_9CAUD	Q77p34 lactococcus
160	36	60.0	252	2	Q94JD6_ORYSA	Q49533 arabidopsis	233	35	58.3	164	2	Q94MA2_9CAUD	Q94ma2 lactococcus
161	36	60.0	253	1	LEP4_VIBCH	Q94jd6 oryza sativ	234	35	58.3	164	2	Q62Y89_BACLD	Q62y89 bacillus l
162	36	60.0	253	2	Q7BG59_VIBCH	P27717 vibrio chol	235	35	58.3	165	2	Q65MU5_BACLD	Q65mu5 bacillus l
163	36	60.0	254	2	Q5BBS2_EMENI	Q7bg59 vibrio chol	236	35	58.3	172	2	Q92TJ5_MAIZE	Q92tj5 zea mays (m
164	36	60.0	282	2	Q5V690_HALMA	Q5bbs2 aspergillus	237	35	58.3	178	2	Q5CXU3_CRYPV	Q5cxu3 cryptospori
165	36	60.0	292	2	Q6SR59_WANSM	Q5v690 haloarcula	238	35	58.3	189	2	Q5CIT2_CRYHO	Q5cit2 cryptospori
166	36	60.0	315	2	Q43888_STRAE	Q6sr59 manniemia	239	35	58.3	202	2	Q8DD99_VIBVU	Q8dd99 vibrio vuln
167	36	60.0	336	2	Q5HL38_STAEO	Q43888 streptococ	240	35	58.3	202	2	Q8B620_VIBVU	Q8b620 vibrio vuln
168	36	60.0	340	2	Q6BLT4_MOUSE	Q5hl38 staphylococ	241	35	58.3	209	2	HOP2_YEAST	HOP2 saccharomyc
169	36	60.0	356	2	Q6AAN6_PROAC	Q6blt4 mus musculu	242	35	58.3	214	2	Q9A0Q2_STRPY	Q9a0q2 streptococ
170	36	60.0	357	2	Q4L307_STAHI	Q6aan6 propionibac	243	35	58.3	215	2	Q5XVL2_BORGA	Q5xvl2 borrelia ga
171	36	60.0	359	2	Q9HL10_THEAC	Q4l307 staphylococ	244	35	58.3	224	2	Q4HE74_CAMVCO	Q4he74 campylobact
172	36	60.0	361	1	SERC_YEREN	Q9hl10 thermoplas	245	35	58.3	231	2	Q72F26_DESVH	Q72f26 desulfovibr
173	36	60.0	361	1	SERC_YERPE	P19689 yersinia en	246	35	58.3	231	2	Q7MGL0_VIBVU	Q7mg10 vibrio vuln
174	36	60.0	361	1	SERC_YERPS	Qzgb4 yersinia pe	247	35	58.3	235	2	Q93VI9_ARATH	Q93vi9 arabidopsis
175	36	60.0	366	2	Q4P4F6_USTMA	Q66ci9 yersinia ps	248	35	58.3	280	1	VPS71_YEAST	VPS71 saccharomyc
176	36	60.0	376	2	Q4P7D0_USTMA	Q4p4t6 ustilago ma	249	35	58.3				
177	36	60.0	385	2	Q4F7D0_USTMA	Q4p7d0 ustilago ma	250	35	58.3				

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:16:43 ; Search time 115.958 Seconds
(without alignments)
66.928 Million cell updates/sec

Title: US-10-091-135-9
Perfect score: 60
Sequence: 1 LKPNCGNKVVV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : UniProt_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	204	1 VA5_VESFL	P35783 vespula fla
2	60	100.0	227	1 VA5_VESVU	Q05110 vespula vul
3	59	98.3	204	1 VA5_VESPE	P35785 vespula pen
4	54	90.0	204	1 VA5_VESMC	P35760 vespula mac
5	48	80.0	204	1 VA5_VESGE	P35784 vespula ger
6	47	78.3	203	1 VA5_DOLAR	Q05108 dolichovesp
7	46	76.7	205	1 VA5_VESSQ	P35786 vespula squ
8	46	76.7	215	1 VA53_DOLMA	P10737 dolichovesp
9	45	75.0	986	2 Q9LYI8_ARATH	Q91137 arabidopsis
10	44	73.3	172	2 Q8PSZ5_METMA	Q8p255 methanogarc
11	44	73.3	694	2 Q9GZ15_DROME	Q9g215 drosophila
12	44	73.3	783	2 Q7KUY7_DROME	Q7kuy7 drosophila
13	44	73.3	840	2 Q9VXL1_DROME	Q9vxl1 drosophila
14	43	71.7	55	2 Q9HKN0_THRAC	Q9hkn0 thermoplasm
15	43	71.7	227	1 VA52_DOLMA	P10736 dolichovesp
16	41	68.3	202	1 VA51_VESCR	P35781 vespa crabr
17	41	68.3	202	1 VA52_VESCR	P35782 vespa crabr
18	41	68.3	202	1 VA5_VESMA	P81657 vespa manda
19	41	68.3	203	2 P97777_RAT	P97777 rattus norv
20	41	68.3	411	2 Q7PSB6_ANOGA	Q7psb6 anopheles g
21	41	68.3	467	1 ADECL1_MOUSE	Q9rx22 mus musculu
22	41	68.3	717	2 Q6S156_ASF	Q6s156 african swi
23	40	66.7	63	2 Q37667_9HIV1	Q37667 human immun
24	40	66.7	184	2 Q5YFD4_9VIRU	Q5yfd4 singapore g
25	40	66.7	201	2 Q6MU65_MYCMS	Q6mu65 mycoplasma
26	40	66.7	206	1 VA5_VESVI	P35787 vespula vid
27	40	66.7	216	2 P90553_9HIV1	P90553 human immun
28	40	66.7	274	2 Q5V6C3_HALMA	Q5v6c3 haloarcula
29	40	66.7	443	2 Q4WDM9_ASPFU	Q4wdm9 aspergillus
30	40	66.7	454	2 Q4L8L4_STAHL	Q4l8l4 staphylococ
31	40	66.7	472	2 Q9W2Y4_DROME	Q9w2y4 drosophila

32	40	66.7	496	2 Q8GHV4_PSERE	Q8ghv4 pseudomonas
33	40	66.7	720	2 Q8XIY0_CLOPE	Q8xiy0 clostridium
34	40	66.7	791	2 Q4I5I6_GIBZE	Q4i5i6 gibberella
35	40	66.7	796	2 Q8A5U3_BACTN	Q8a5u3 bacteroides
36	40	66.7	798	2 Q64PL2_BACFR	Q64pl2 bacteroides
37	40	66.7	864	2 Q4UEY4_THEAN	Q4uey4 theileria a
38	40	66.7	882	2 Q5L9C8_BACFN	Q5l9c8 bacteroides
39	40	66.7	1011	2 Q9BXK2_HUMAN	Q9bxk2 homo sapien
40	40	66.7	1196	2 Q8BGG7_PARTE	Q8bgg7 paramecium
41	40	66.7	1313	2 Q54FD2_DICDI	Q54fd2 dictyosteli
42	39.5	65.8	1312	2 Q6BIP6_DEBHA	Q6bip6 debaryomyce
43	39	65.0	60	2 Q7USL7_RHOBA	Q7usl7 rhodospirell
44	39	65.0	146	2 Q9LYV7_ARATH	Q9lyv7 arabidopsis
45	39	65.0	235	2 Q5WTB6_LRGPL	Q5wtb6 legionella
46	39	65.0	235	2 Q5XIK7_LEGPA	Q5xik7 legionella
47	39	65.0	245	2 Q7ID91_DROYA	Q7id91 drosophila
48	39	65.0	247	2 Q9XIS9_THEMEA	Q9xis9 thermocoga
49	39	65.0	323	2 Q5OV00_ENTHI	Q5ov00 entamoeba h
50	39	65.0	344	2 Q6TVK6_9POXV	Q6tvk6 orf virus.
51	39	65.0	346	2 Q6TVV6_9POXV	Q6tvv6 orf virus.
52	39	65.0	351	2 Q9UX43_SULSO	Q9ux43 sulfolobus
53	39	65.0	437	2 Q54C11_DICDI	Q54c11 dictyosteli
54	39	65.0	460	1 SYG_STRAC	Q82br9 streptomyce
55	39	65.0	460	1 SYG_PROAC	Q912h9 streptomyce
56	39	65.0	472	1 SYG_PROAC	Q8a964 propionibac
57	39	65.0	599	2 Q86GD7_CRAGI	Q86gd7 crassostrea
58	39	65.0	627	2 Q6U9G1_9CAUD	Q6u9g1 bacterioph
59	39	65.0	627	2 Q56EM2_9CAUD	Q56em2 aeromonas p
60	39	65.0	819	1 ADAM9_HUMAN	Q13443 homo sapien
61	39	65.0	845	1 ADAM9_MOUSE	Q61072 mus musculu
62	39	65.0	845	2 Q58GH2_RAT	Q58gh2 rattus norv
63	39	65.0	2072	2 Q7RSW8_PLAYO	Q7rsw8 plasmodium
64	38	63.3	72	2 Q4V110_BACCC	Q4v110 bacillus ce
65	38	63.3	116	2 Q4WJD3_ASPFU	Q4wjd3 aspergillus
66	38	63.3	182	2 Q65JE3_BACLD	Q65je3 bacillus li
67	38	63.3	295	2 Q9HEH0_NEUCR	Q9heh0 neurospora
68	38	63.3	323	2 Q34789_BACSU	Q34789 bacillus su
69	38	63.3	324	2 Q65MY2_BACLD	Q65my2 bacillus li
70	38	63.3	356	1 Y1773_VIBCH	Q9kr70 vibrio chol
71	38	63.3	376	2 Q7PVP3_ANOGA	Q7pvp3 anopheles g
72	38	63.3	384	2 Q51IL2_MAGGR	Q51il2 magnaporthe
73	38	63.3	385	2 Q972Z1_SULTO	Q972z1 sulfolobus
74	38	63.3	391	2 Q7PVP2_ANOGA	Q7pvp2 anopheles g
75	38	63.3	469	2 Q5N3X4_SINP6	Q5n3x4 synecococc
76	38	63.3	697	2 Q9VU11_DROME	Q9vu11 drosophila
77	38	63.3	823	2 Q6LYN4_METMP	Q6lyn4 methanococ
78	38	63.3	1169	2 Q6ZQH3_MOUSE	Q6zqh3 mus musculu
79	38	63.3	1622	2 Q5R888_PONPY	Q5r888 pongo pygma
80	38	63.3	1753	2 Q7LE74_MOUSE	Q7le74 mus musculu
81	38	63.3	2067	1 NCOA6_MOUSE	Q9j119 m nuclear r
82	38	63.3	2069	2 Q5XJV5_MOUSE	Q5xjv5 mus musculu
83	38	63.3	2151	2 Q9NG79_TRIVA	Q9ng79 trichomonas
84	38	63.3	2511	2 Q8IL44_PLAF7	Q8il44 plasmodium
85	38	63.3	2623	2 Q54SZ1_DICDI	Q54sz1 dictyosteli
86	38	63.3	4483	2 Q5IQB7_MAGGR	Q5iqb7 magnaporthe
87	37	61.7	66	1 RS27_SULTO	Q973f9 sulfolobus
88	37	61.7	67	2 Q7VNL5_HAEDU	Q7vnl5 haemophilus
89	37	61.7	115	2 Q9M5V2_SOYBN	Q9m5v2 glycine max
90	37	61.7	126	2 Q5TG92_HUMAN	Q5tg92 homo sapien
91	37	61.7	134	2 Q9ACD4_ARATH	Q9acd4 arabidopsis
92	37	61.7	149	2 Q725D6_LISMF	Q725d6 listeria mo
93	37	61.7	156	2 Q20386_CABEL	Q20386 caenorhabdi
94	37	61.7	175	2 Q899U7_CLOTE	Q899u7 clostridium
95	37	61.7	181	1 COTE_BACSU	P14016 bacillus su
96	37	61.7	182	2 Q5L0E6_GROKA	Q5l0e6 geobacillus
97	37	61.7	206	2 Q9K4H7_STRCO	Q9k4h7 streptomyce
98	37	61.7	208	2 Q4QJQ5_AZQVI	Q4jq5 azotobacter
99	37	61.7	295	1 Y851_PYRPU	Q8u1r0 pyrococcus
100	37	61.7	295	1 Y851_PYRPU	Q9v0d9 pyrococcus
101	37	61.7	295	1 Y851_PYRPU	Q58667 pyrococcus
102	37	61.7	347	2 Q5FIM6_LACAC	Q5fim6 lactobacill
103	37	61.7	369	2 Q6ZB86_ORYSA	Q6zb86 oryza sativ
104	37	61.7	386	2 O50729_BORBU	O50729 borrella bu

103	34	56.7	616	2	A99969	anaerobic ribonuc	176	33	55.0	1221	2	T18550	reverse gyrase cha
104	34	56.7	641	2	AD1724	NADH oxidase homol	177	33	55.0	1239	2	T13809	probable disintegr
105	34	56.7	735	2	E95023	anaerobic ribonuc	178	32.5	54.2	66	2	H70077	hypothetical prote
106	34	56.7	737	2	G97894	ribonucleoside-tri	179	32	53.3	96	2	T45855	hypothetical prote
107	34	56.7	750	2	A56881	prostate-specific	180	32	53.3	106	2	E71618	Zn-ribbon transcri
108	34	56.7	765	2	G96896	protein FLN21.14 [181	32	53.3	111	2	F56556	fork head homolog
109	34	56.7	787	2	C84998	hypothetical prote	182	32	53.3	124	2	T26799	hypothetical prote
110	34	56.7	835	2	T05259	probable disease r	183	32	53.3	128	2	T40344	hypothetical zinc
111	34	56.7	878	2	F64425	valine-tRNA ligase	184	32	53.3	130	2	D84363	hypothetical prote
112	34	56.7	1048	1	XPB2A9	large structural p	185	32	53.3	153	2	AF1908	probable exported
113	34	56.7	1056	2	T00060	hypothetical prote	186	32	53.3	159	2	AI0772	185K secretory pro
114	34	56.7	1369	2	S58160	hypothetical prote	187	32	53.3	160	2	JQ0542	serine O-acetyltra
115	34	56.7	1503	2	T43166	alpha-2-macroglobu	188	32	53.3	171	1	B64671	o-serine acetyltra
116	34	56.7	2212	2	A41098	calcium channel pr	189	32	53.3	171	2	B71845	hypothetical prote
117	34	56.7	3759	2	A35085	trithorax protein	190	32	53.3	181	2	E36794	GTP-binding protei
118	34	56.7	3828	2	T13857	trithorax protein	191	32	53.3	215	2	F34323	hypothetical prote
119	33.5	55.8	602	2	T47794	hypothetical prote	192	32	53.3	221	2	F84431	hypothetical prote
120	33	55.0	55	2	F82658	hypothetical prote	193	32	53.3	236	2	T45067	hypothetical prote
121	33	55.0	57	2	G64372	hypothetical prote	194	32	53.3	245	2	T51276	hypothetical prote
122	33	55.0	61	2	A64392	hypothetical prote	195	32	53.3	259	2	F64532	conserved hypotet
123	33	55.0	114	2	S70116	hypothetical prote	196	32	53.3	260	2	E71975	hypothetical prote
124	33	55.0	123	2	AC2234	hypothetical prote	197	32	53.3	271	2	S27422	peroxisomal assem
125	33	55.0	138	2	G40605	response regulator	198	32	53.3	294	2	G90032	hypothetical prote
126	33	55.0	146	2	B84180	hypothetical prote	200	32	53.3	305	2	S29711	oligofactor O
127	33	55.0	157	2	T28321	ORF MSV160 hypote	201	32	53.3	313	2	G81782	adhesin MafA2 NMA2
128	33	55.0	158	2	D90391	conserved hypotet	202	32	53.3	314	2	G81173	adhesin mafa - Nel
129	33	55.0	161	2	F71117	hypothetical prote	203	32	53.3	314	1	G64658	probable pyruvate
130	33	55.0	211	2	T48794	hypothetical prote	204	32	53.3	330	2	A71858	pyruvate ferredoxi
131	33	55.0	230	2	T26896	hypothetical prote	205	32	53.3	334	2	G90256	DNA primase, proba
132	33	55.0	241	1	ZQBPWQ	mem protein - phag	206	32	53.3	347	2	D96590	hypothetical prote
133	33	55.0	250	2	AB0421	PNP protein [impo	207	32	53.3	362	1	E64187	phosphoserine tran
134	33	55.0	279	2	T16014	hypothetical prote	208	32	53.3	365	2	E90099	hypothetical prote
135	33	55.0	332	1	A55897	prolactin-induced	209	32	53.3	370	2	S29139	aggreccan - pig (fr
136	33	55.0	342	1	G70460	conserved hypotet	210	32	53.3	374	2	E83894	hypothetical prote
137	33	55.0	370	2	A72572	hypothetical prote	211	32	53.3	375	2	E85035	hypothetical prote
138	33	55.0	402	2	D70186	xylose operon regu	212	32	53.3	377	2	T06643	zinc metalloprotei
139	33	55.0	404	2	C81274	hypothetical prote	213	32	53.3	387	2	E96724	hypothetical prote
140	33	55.0	409	2	S55178	probable sphingoli	214	32	53.3	397	2	T19370	hypothetical prote
141	33	55.0	464	2	S50592	hypothetical prote	215	32	53.3	405	2	C82168	hypothetical prote
142	33	55.0	470	2	T16606	probable serine ca	216	32	53.3	425	2	T48993	hypothetical prote
143	33	55.0	474	1	IMBP4	site-specific reco	217	32	53.3	428	2	T39773	hypothetical prote
144	33	55.0	500	1	S02302	aldehyde dehydroge	218	32	53.3	433	1	S48515	adenylosuccinate s
145	33	55.0	501	1	DEHUE1	aldehyde dehydroge	219	32	53.3	465	2	C84083	hypothetical prote
146	33	55.0	501	1	JQ1004	aldehyde dehydroge	220	32	53.3	471	2	T26612	hypothetical prote
147	33	55.0	501	2	S14752	aldehyde dehydroge	221	32	53.3	474	2	T27006	hypothetical prote
148	33	55.0	501	2	JC4534	aldehyde dehydroge	222	32	53.3	481	2	S62427	G-protein signalin
149	33	55.0	501	2	JC5553	aldehyde dehydroge	223	32	53.3	486	2	S10772	2-hydroxymuconic s
150	33	55.0	540	2	A71610	HSP60 fold T-compl	224	32	53.3	491	2	H84840	hypothetical prote
151	33	55.0	544	2	S26425	site-specific DNA-	225	32	53.3	493	2	I38621	actin bundling pro
152	33	55.0	569	2	H87926	protein C17D12.7 [226	32	53.3	501	1	A32616	aldehyde dehydroge
153	33	55.0	594	2	T23841	hypothetical prote	227	32	53.3	505	2	T31272	4-carboxy-2-hydrox
154	33	55.0	600	2	T49281	fertilin alpha pre	228	32	53.3	506	2	S58150	hypothetical prote
155	33	55.0	610	2	T23836	hypothetical prote	229	32	53.3	509	1	S14629	aldehyde dehydroge
156	33	55.0	630	2	D97992	hypothetical prote	230	32	53.3	518	2	E84536	hypothetical prote
157	33	55.0	641	2	AC1354	NADH oxidase homol	231	32	53.3	525	2	T20662	hypothetical prote
158	33	55.0	657	2	T48228	probable protein k	232	32	53.3	543	2	I40545	oligopeptide ABC t
159	33	55.0	660	2	A28153	gelatinase A (EC 3	233	32	53.3	546	2	T40258	probable t-complex
160	33	55.0	662	2	S70365	gelatinase A (EC 3	234	32	53.3	557	2	T43202	probable chaperoni
161	33	55.0	662	2	A42486	gelatinase A (EC 3	235	32	53.3	572	2	T40856	probable nucleotid
162	33	55.0	662	2	S34780	gelatinase A (EC 3	236	32	53.3	616	1	RRVQLL	probable RNA-direc
163	33	55.0	663	1	S46492	gelatinase A (EC 3	237	32	53.3	638	1	RRVQWA	probable RNA-direc
164	33	55.0	669	2	T16626	hypothetical prote	238	32	53.3	639	2	AC2895	conserved hypotet
165	33	55.0	709	2	E64213	DNA topoisomerase	239	32	53.3	657	2	T41546	beta-N-acetylhexos
166	33	55.0	718	1	A69084	SHE4 protein - yea	240	32	53.3	663	1	E69475	beta-N-acetylhexos
167	33	55.0	789	2	S62172	exoribonuclease RN	241	32	53.3	697	2	C97120	DNA topoisomerase I [1
168	33	55.0	793	2	AI1380	exoribonuclease RN	242	32	53.3	751	1	I49497	transforming prote
169	33	55.0	793	2	AB1750	exoribonuclease RN	243	32	53.3				
170	33	55.0	832	2	G97146	probable permease	244	32	53.3				
171	33	55.0	977	2	S62540	hypothetical prote	245	32	53.3				
172	33	55.0	1092	2	H69071	DNA-directed DNA p	246	32	53.3				
173	33	55.0	1146	2	B70376	reverse gyrase - A	247	32	53.3				
174	33	55.0	1156	2	T23748	hypothetical prote	248	32	53.3				
175	33	55.0	1207	2	T23754	hypothetical prote							

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:19:39 ; Search time 18.3333 Seconds
(without alignments)
57.730 Million cell updates/sec

Title: US-10-091-135-9
Perfect score: 60
Sequence: 1 LKPNCGNKVVV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	204	A44583	venom allergen ant
2	59	98.3	204	C44583	venom allergen ant
3	54	90.0	204	B37329	antigen 5 - easter
4	48	80.0	204	B44583	venom allergen ant
5	48	80.0	213	B31085	antigen 5-3 precu
6	46	76.7	205	D44583	venom allergen ant
7	45	75.0	886	T48544	MAP3K delta-1 prot
8	43	71.7	227	A31085	antigen 5-2 precu
9	41	68.3	202	H44583	venom allergen ant
10	41	68.3	202	G44583	venom allergen ant
11	40	66.7	206	E44583	venom allergen ant
12	39	65.0	146	T48566	hypothetical prote
13	39	65.0	247	E72233	conserved hypothet
14	39	65.0	351	G90212	conserved hypothet
15	39	65.0	655	JC7850	disintegrin and me
16	39	65.0	660	S71949	metalloproteinase
17	38	63.3	323	E69789	hypothetical prote
18	38	63.3	356	B82159	conserved hypothet
19	37	61.7	142	T22156	hypothetical prote
20	37	61.7	181	A31245	outer spore coat p
21	37	61.7	295	D75131	mrp-family probabl
22	37	61.7	295	D71085	probable MRP prote
23	37	61.7	386	F70231	conserved hypothet
24	37	61.7	653	I48341	endoglin - mouse
25	37	61.7	829	S50246	SIP4 protein - yea
26	36	60.0	66	B90257	SSU ribosomal prot
27	36	60.0	73	G72737	probable ribosomal
28	36	60.0	180	C97050	phage related prot
29	36	60.0	244	T01761	hypothetical prote

30	36	60.0	253	1	A40582	type IV preplin p
31	36	60.0	253	2	D82273	leader peptidase T
32	36	60.0	315	2	I39479	hypothetical prote
33	36	60.0	361	1	XNEBPY	phosphoserine tran
34	36	60.0	361	2	AG0169	phosphoserine tran
35	36	60.0	459	2	T27657	hypothetical prote
36	36	60.0	571	2	H97333	site-specific modi
37	36	60.0	576	2	S75958	hypothetical prote
38	36	60.0	644	2	AB1486	transcription anti
39	36	60.0	714	2	S68603	hypothetical prote
40	36	60.0	842	2	B97337	ABC-type transport
41	36	60.0	891	2	T19915	hypothetical prote
42	36	60.0	934	2	T39941	hypothetical prote
43	35	58.3	105	2	B71081	hypothetical prote
44	35	58.3	109	2	T38145	DNA-directed RNA p
45	35	58.3	116	2	I84704	gene VHL04B protei
46	35	58.3	201	2	B69546	conserved hypothet
47	35	58.3	202	2	T05763	hypothetical prote
48	35	58.3	280	2	S52479	hypothetical prote
49	35	58.3	323	2	T01626	peroxidase (EC 1.1
50	35	58.3	325	2	T14077	peroxidase (EC 1.1
51	35	58.3	329	2	T04710	peroxidase (EC 1.1
52	35	58.3	329	2	T04709	peroxidase (EC 1.1
53	35	58.3	357	2	A86825	hypothetical prote
54	35	58.3	384	2	C82159	conserved hypothet
55	35	58.3	484	2	G86362	beta-glucanase (im
56	35	58.3	679	2	S64258	hypothetical prote
57	35	58.3	1312	2	T32758	hypothetical prote
58	35	58.3	1463	2	C95032	DNA-directed DNA p
59	35	58.3	1463	2	C97903	voltage-gated sodi
60	35	58.3	1695	2	JE0084	aggreasin precursor
61	35	58.3	2109	1	I50421	arietin - puff add
62	34	56.7	30	2	S15982	hypothetical prote
63	34	56.7	50	2	E82816	hypothetical prote
64	34	56.7	81	2	AC3489	bitan alpha - puff
65	34	56.7	83	2	F35982	hypothetical prote
66	34	56.7	84	2	S42603	hypothetical prote
67	34	56.7	85	2	AB2872	conserved hypothet
68	34	56.7	85	2	E97648	hypothetical prote
69	34	56.7	109	2	F90242	hypothetical prote
70	34	56.7	188	2	T51271	conserved hypothet
71	34	56.7	210	2	T45903	hypothetical prote
72	34	56.7	254	2	F69547	nucleotide-binding
73	34	56.7	254	2	A95216	type II restrictio
74	34	56.7	254	2	A31975	endonuclease dpnc
75	34	56.7	254	2	G98079	type II site-speci
76	34	56.7	256	2	G96692	hypothetical prote
77	34	56.7	258	2	T32542	hypothetical prote
78	34	56.7	266	2	C72380	hypothetical prote
79	34	56.7	294	2	S73232	ribosomal protein
80	34	56.7	317	2	S76723	hypothetical prote
81	34	56.7	322	2	D86228	hypothetical prote
82	34	56.7	324	2	T46213	hypothetical prote
83	34	56.7	331	2	C72339	hypothetical prote
84	34	56.7	350	2	A64813	vhbH protein - Esc
85	34	56.7	350	2	F85579	hypothetical prote
86	34	56.7	350	2	E90728	hypothetical prote
87	34	56.7	359	2	D96910	muconate cycloisom
88	34	56.7	365	2	AC3080	conserved hypothet
89	34	56.7	365	2	F98206	hypothetical 37.1K
90	34	56.7	389	1	SVPIJCF	navingenin-chalcon
91	34	56.7	391	2	T14580	SIP4 protein pre
92	34	56.7	406	2	AC2007	transposase allr60
93	34	56.7	406	2	A12497	transposase allr716
94	34	56.7	411	2	B91220	probable arylsulfat
95	34	56.7	411	2	D86066	probable arylsulfat
96	34	56.7	411	2	A65184	arylsulfatase aci
97	34	56.7	448	2	T29040	hypothetical prote
98	34	56.7	473	2	I49283	ADAM 4 protein pre
99	34	56.7	473	2	A86442	hypothetical prote
100	34	56.7	493	2	T12304	catalase (EC 1.1.1
101	34	56.7	583	2	A85588	hypothetical prote
102	34	56.7	583	2	H90737	hypothetical prote

98	37	61.7	185	4	AAB63933	Aab63933 Human pro	171	37	61.7	3843	4	ABB71529	Abb71529 Drosophila
99	37	61.7	189	4	AAB63929	Aab63929 Human pro	172	36	60.0	62	4	AM20362	Am20362 Peptide #
100	37	61.7	195	4	AAB63918	Aab63918 Human pro	173	36	60.0	62	4	AB40953	Ab40953 Peptide #
101	37	61.7	207	4	AAB63937	Aab63937 Human pro	174	36	60.0	62	4	AB34727	Ab34727 Peptide #
102	37	61.7	220	4	AAB63917	Aab63917 Human pro	175	36	60.0	62	4	AB25065	Ab25065 Protein #
103	37	61.7	223	4	AAB63903	Aab63903 Human pro	176	36	60.0	62	4	AM74616	Am74616 Human bon
104	37	61.7	225	4	AAB63901	Aab63901 Human pro	177	36	60.0	62	4	AM61815	Am61815 Human liv
105	37	61.7	229	4	AAB63925	Aab63925 Human pro	178	36	60.0	62	4	ABG56400	Abg56400 Human liv
106	37	61.7	241	7	ADB83989	Aab63925 Human pro	179	36	60.0	62	5	ABG44443	Abg44443 Human pap
107	37	61.7	266	4	AAB63899	Aab63899 Human pro	180	36	60.0	102	2	AAW98755	Aaw98755 H. pylori
108	37	61.7	325	4	ABX1828	Adx1828 Plant ful	181	36	60.0	125	3	AAW96731	Aaw96731 PRO982, a
109	37	61.7	343	8	ADY1286	Ady1286 Bacterial	182	36	60.0	125	3	AAW96731	Aaw96731 PRO982, a
110	37	61.7	390	8	ADY1286	Ady1286 Bacterial	183	36	60.0	125	3	AAW96731	Aaw96731 PRO982, a
111	37	61.7	394	5	ABP73544	Abp73544 Candida a	184	36	60.0	125	4	ABG50956	Abg50956 Human PRO
112	37	61.7	398	3	ABP7638	Abp7638 Amino aci	185	36	60.0	125	4	ABG50956	Abg50956 Human PRO
113	37	61.7	445	4	AAB50249	Aab50249 Human bre	186	36	60.0	125	4	ABG50956	Abg50956 Human PRO
114	37	61.7	445	4	AAG65987	Aag65987 B726P spl	187	36	60.0	125	5	ABG81276	Abg81276 Human PRO
115	37	61.7	445	4	AAU33350	Aau33350 Human bre	188	36	60.0	125	5	ABG81276	Abg81276 Human PRO
116	37	61.7	445	5	ABG78917	Abg78917 Human bre	189	36	60.0	125	5	ABG81276	Abg81276 Human PRO
117	37	61.7	445	6	ABJ37740	Abj37740 Human tum	190	36	60.0	125	5	ABG81276	Abg81276 Human PRO
118	37	61.7	445	7	ADL93135	Adl93135 Human bre	191	36	60.0	125	5	ABG81276	Abg81276 Human PRO
119	37	61.7	445	8	ADL44425	Adl44425 Human bre	192	36	60.0	125	5	ABG81276	Abg81276 Human PRO
120	37	61.7	466	4	AAB50248	Aab50248 Human bre	193	36	60.0	125	5	ABG81276	Abg81276 Human PRO
121	37	61.7	466	4	AAG65986	Aag65986 B726P spl	194	36	60.0	125	5	ABG81276	Abg81276 Human PRO
122	37	61.7	466	4	AAU33349	Aau33349 Human bre	195	36	60.0	125	5	ABG81276	Abg81276 Human PRO
123	37	61.7	466	5	ABG78916	Abg78916 Human bre	196	36	60.0	125	5	ABG81276	Abg81276 Human PRO
124	37	61.7	466	6	ABJ37739	Abj37739 Human tum	197	36	60.0	125	5	ABG81276	Abg81276 Human PRO
125	37	61.7	466	7	ADL93134	Adl93134 Human bre	198	36	60.0	125	5	ABG81276	Abg81276 Human PRO
126	37	61.7	466	8	ADE44424	Ade44424 Human bre	199	36	60.0	125	5	ABG81276	Abg81276 Human PRO
127	37	61.7	650	4	AAB50263	Aab50263 Human bre	200	36	60.0	125	5	ABG81276	Abg81276 Human PRO
128	37	61.7	650	4	AAG65983	Aag65983 B726P spl	201	36	60.0	125	5	ABG81276	Abg81276 Human PRO
129	37	61.7	650	4	AAU33346	Aau33346 Human bre	202	36	60.0	125	5	ABG81276	Abg81276 Human PRO
130	37	61.7	650	5	ABG78913	Abg78913 Human bre	203	36	60.0	125	5	ABG81276	Abg81276 Human PRO
131	37	61.7	650	6	ABJ37736	Abj37736 Human tum	204	36	60.0	125	5	ABG81276	Abg81276 Human PRO
132	37	61.7	650	7	ADL93131	Adl93131 Human bre	205	36	60.0	125	5	ABG81276	Abg81276 Human PRO
133	37	61.7	650	8	ADE44421	Ade44421 Human bre	206	36	60.0	125	5	ABG81276	Abg81276 Human PRO
134	37	61.7	653	5	ADL17107	Adl17107 Murine NO	207	36	60.0	125	5	ABG81276	Abg81276 Human PRO
135	37	61.7	661	6	ABJ37782	Abj37782 Human tum	208	36	60.0	125	5	ABG81276	Abg81276 Human PRO
136	37	61.7	661	7	ADL93214	Adl93214 Human bre	209	36	60.0	125	5	ABG81276	Abg81276 Human PRO
137	37	61.7	710	7	ABM85466	Abm85466 Mouse pro	210	36	60.0	125	5	ABG81276	Abg81276 Human PRO
138	37	61.7	713	4	AAU33358	Aau33358 Human bre	211	36	60.0	125	5	ABG81276	Abg81276 Human PRO
139	37	61.7	743	5	ABG78925	Abg78925 Human bre	212	36	60.0	125	5	ABG81276	Abg81276 Human PRO
140	37	61.7	743	6	ABJ37748	Abj37748 Human tum	213	36	60.0	125	5	ABG81276	Abg81276 Human PRO
141	37	61.7	743	7	ADL93156	Adl93156 Human bre	214	36	60.0	125	5	ABG81276	Abg81276 Human PRO
142	37	61.7	829	5	ABP35670	Abp35670 Fungal 2B	215	36	60.0	125	5	ABG81276	Abg81276 Human PRO
143	37	61.7	829	8	ADT87129	Adt87129 Yeast Str	216	36	60.0	125	5	ABG81276	Abg81276 Human PRO
144	37	61.7	1002	4	AAU33351	Aau33351 Human bre	217	36	60.0	125	5	ABG81276	Abg81276 Human PRO
145	37	61.7	1002	5	ABG78918	Abg78918 Human bre	218	36	60.0	125	5	ABG81276	Abg81276 Human PRO
146	37	61.7	1002	6	ABJ37741	Abj37741 Human tum	219	36	60.0	125	5	ABG81276	Abg81276 Human PRO
147	37	61.7	1002	7	ADL93137	Adl93137 Human bre	220	36	60.0	125	5	ABG81276	Abg81276 Human PRO
148	37	61.7	1002	8	ADE44427	Ade44427 Human bre	221	36	60.0	125	5	ABG81276	Abg81276 Human PRO
149	37	61.7	1013	6	ABJ37783	Abj37783 Human tum	222	36	60.0	125	5	ABG81276	Abg81276 Human PRO
150	37	61.7	1013	7	ADL93215	Adl93215 Human bre	223	36	60.0	125	5	ABG81276	Abg81276 Human PRO
151	37	61.7	1030	6	ABU20850	Abu20850 Protein e	224	36	60.0	125	5	ABG81276	Abg81276 Human PRO
152	37	61.7	1095	4	AAU33357	Aau33357 Human bre	225	36	60.0	125	5	ABG81276	Abg81276 Human PRO
153	37	61.7	1095	5	ABG78924	Abg78924 Human bre	226	36	60.0	125	5	ABG81276	Abg81276 Human PRO
154	37	61.7	1095	6	ABJ37747	Abj37747 Human tum	227	36	60.0	125	5	ABG81276	Abg81276 Human PRO
155	37	61.7	1095	7	ADL93155	Adl93155 Human bre	228	36	60.0	125	5	ABG81276	Abg81276 Human PRO
156	37	61.7	1191	5	AAU98061	Aau98061 Bacillus	229	36	60.0	125	5	ABG81276	Abg81276 Human PRO
157	37	61.7	1339	9	AEA20113	Aea20113 Novel hum	230	36	60.0	125	5	ABG81276	Abg81276 Human PRO
158	37	61.7	1341	4	AAB84702	Aab84702 Amino aci	231	36	60.0	125	5	ABG81276	Abg81276 Human PRO
159	37	61.7	1341	5	ABJ05537	Abj05537 Breast ca	232	36	60.0	125	5	ABG81276	Abg81276 Human PRO
160	37	61.7	1341	6	ABJ37784	Abj37784 Human tum	233	36	60.0	125	5	ABG81276	Abg81276 Human PRO
161	37	61.7	1341	7	ABR47548	Abra47548 Breast ca	234	36	60.0	125	5	ABG81276	Abg81276 Human PRO
162	37	61.7	1341	8	ADL93227	Adl93227 Human bre	235	36	60.0	125	5	ABG81276	Abg81276 Human PRO
163	37	61.7	1341	9	ADT49017	Adt49017 Human BFA	236	36	60.0	125	5	ABG81276	Abg81276 Human PRO
164	37	61.7	1341	10	ADU99254	Adu99254 BFA5 tumo	237	36	60.0	125	5	ABG81276	Abg81276 Human PRO
165	37	61.7	1341	11	ADV60459	Adv60459 Human bre	238	36	60.0	125	5	ABG81276	Abg81276 Human PRO
166	37	61.7	1341	12	ADY93219	Ady93219 Human NY-	239	36	60.0	125	5	ABG81276	Abg81276 Human PRO
167	37	61.7	1349	6	ABJ37788	Abj37788 Human tum	240	36	60.0	125	5	ABG81276	Abg81276 Human PRO
168	37	61.7	1349	7	ADL93235	Adl93235 Human bre	241	36	60.0	125	5	ABG81276	Abg81276 Human PRO
169	37	61.7	1397	9	ADY93228	Ady93228 Human NY-	242	36	60.0	125	5	ABG81276	Abg81276 Human PRO
170	37	61.7	1432	6	ABU24715	Abu24715 Protein e	243	36	60.0	125	5	ABG81276	Abg81276 Human PRO

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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:13:51 ; Search time 96.7083 Seconds
(without alignments)
49.977 Million cell updates/sec

Title: US-10-091-135-9
Perfect score: 60
Sequence: 1 LKPCNGKVVV 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A_Geneseq_21:*

- 1: Geneseqp1980s:*
- 2: Geneseqp1990s:*
- 3: Geneseqp2000s:*
- 4: Geneseqp2001s:*
- 5: Geneseqp2002s:*
- 6: Geneseqp2003as:*
- 7: Geneseqp2003bs:*
- 8: Geneseqp2004s:*
- 9: Geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	60	100.0	11	5	Aae28815 Vespula v
2	60	100.0	32	5	Aae28810 Vespula v
3	60	100.0	39	5	Aae28811 Vespula v
4	60	100.0	46	5	Aae28812 Vespula v
5	60	100.0	50	5	Aae28827 Vespula v
6	60	100.0	57	5	Aae28828 Vespula v
7	60	100.0	76	5	Aae28829 Vespula v
8	60	100.0	204	2	Aay45217 Wild type
9	60	100.0	204	2	Aay45217 Wild type
10	60	100.0	204	5	ABG66983 Wasp veno
11	60	100.0	204	5	ABG67052 Wasp veno
12	60	100.0	204	5	ABG67104 Wasp veno
13	60	100.0	204	5	ABG67103 Wasp veno
14	60	100.0	204	5	Aae28820 Vespula v
15	60	100.0	209	4	ABM00031 Allergen
16	60	100.0	227	2	Aay25644 Vespula s
17	60	100.0	227	4	Aae13071 Vespula v
18	60	100.0	227	7	Adc34893 Wasp alle
19	56	93.3	31	2	Aaw35648 T cell pe
20	54	90.0	204	2	Aaw35687 Vespul an
21	54	90.0	204	5	ABG66977 Wasp veno
22	50	83.3	31	2	Aaw35647 T cell pe
23	48	80.0	32	2	Aaw35650 T cell pe
24	48	80.0	205	2	Aaw35690 Vespul an

25	47	78.3	31	2	AAW35649	2	AAW35649	T cell pe
26	47	78.3	203	2	AAW35689	2	AAW35689	Vespul an
27	44	73.3	685	4	ABB64268	4	ABB64268	Drosophil
28	43	71.7	32	2	AAW35694	2	AAW35694	D. macula
29	43	71.7	32	2	AAW35651	2	AAW35651	T cell pe
30	43	71.7	204	2	AAW35691	2	AAW35691	Vespul an
31	40	66.7	206	2	AAW25648	2	AAW25648	Vespula s
32	40	66.7	206	7	ADC34897	7	ADC34897	Wasp alle
33	40	66.7	473	4	ABB58662	4	ABB58662	Drosophil
34	40	66.7	1011	4	AAW35651	4	AAW35651	Amino aci
35	40	66.7	1011	7	ADJ69751	7	ADJ69751	Human hea
36	40	66.7	1011	9	ADY93223	9	ADY93223	Human NY-
37	40	66.7	1225	6	ABR47547	6	ABR47547	Breast ca
38	40	66.7	1239	6	ABJ37789	6	ABJ37789	Human tum
39	40	66.7	1239	7	ADL93239	7	ADL93239	Human bre
40	39	65.0	20	2	AAW35620	2	AAW35620	Immunomod
41	39	65.0	32	2	AAW35644	32	AAW35644	Immunomod
42	39	65.0	130	5	ABP04459	5	ABP04459	Human ORF
43	39	65.0	223	4	AAU64792	4	AAU64792	Propionib
44	39	65.0	223	6	ABM61311	6	ABM61311	Propionib
45	39	65.0	235	9	ABE33340	9	ABE33340	L. pneumo
46	39	65.0	239	9	ABE33905	9	ABE33905	L. pneumo
47	39	65.0	322	2	AAW25723	2	AAW25723	Human par
48	39	65.0	358	6	ABM64563	6	ABM64563	Propionib
49	39	65.0	383	5	AAO14382	5	AAO14382	Human met
50	39	65.0	436	6	ABR41539	6	ABR41539	Human DIT
51	39	65.0	631	4	AGW73908	4	AGW73908	Human col
52	39	65.0	631	6	ABU04241	6	ABU04241	Human exp
53	39	65.0	660	2	AAW44120	2	AAW44120	Human ADA
54	39	65.0	660	5	AAO14370	5	AAO14370	Human met
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57	39	65.0	818	8	ADR66829	8	ADR66829	Human pro
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59	39	65.0	818	8	ADU97559	8	ADU97559	Panccreat
60	39	65.0	819	5	AAU76355	5	AAU76355	Human ADA
61	39	65.0	819	6	ABU56717	6	ABU56717	Lung canc
62	39	65.0	819	6	ABU04239	6	ABU04239	Human exp
63	39	65.0	819	6	ABU04243	6	ABU04243	Human exp
64	39	65.0	819	6	ABU04244	6	ABU04244	Human exp
65	39	65.0	819	7	ADN39132	7	ADN39132	Cancer/an
66	39	65.0	819	7	ADP65169	7	ADP65169	Human a d
67	39	65.0	819	8	ADF42804	8	ADF42804	Human MDC
68	39	65.0	819	8	ADN32830	8	ADN32830	Amino aci
69	39	65.0	819	8	ADO50406	8	ADO50406	Human ADA
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71	39	65.0	819	9	ADU19768	9	ADU19768	PRO poly
72	39	65.0	819	9	ADY30226	9	ADY30226	Human ADA
73	39	65.0	827	6	ABU11697	6	ABU11697	Human MDD
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77	39	65.0	845	5	ABW57371	5	ABW57371	Mouse lsc
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83	38	63.3	517	5	ABG80401	5	ABG80401	Megasphae
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93	37	61.7	134	3	AAW57552	3	AAW57552	Arabidops
94	37	61.7	168	4	ABW63909	4	ABW63909	Human pro
95	37	61.7	169	4	ABW63906	4	ABW63906	Human pro
96	37	61.7	174	4	ABW63926	4	ABW63926	Human pro
97	37	61.7	174	4	ABW63926	4	ABW63926	Human pro

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:08:42 ; Search time 12.1565 Seconds
(without alignments)
171.264 Million cell updates/sec

Title: US-10-091-135-8
Perfect score: 285
Sequence: 1 HYTMWANTKEVCGSGSIKY.....LVCNYGSPGNFKNEELYQTK 49

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA New: *
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4: /SID55/ptodata/2/pubpaa/PCT_NEW_PUB.pep: *
5: /SID55/ptodata/2/pubpaa/US09_NEW_PUB.pep: *
6: /SID55/ptodata/2/pubpaa/US10_NEW_PUB.pep: *
7: /SID55/ptodata/2/pubpaa/US11_NEW_PUB.pep: *
8: /SID55/ptodata/2/pubpaa/US60_NEW_PUB.pep: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	279	97.9	227	6	US-10-498-026-76
2	237	83.2	206	6	US-10-498-026-80
3	123	43.2	270	6	US-10-986-405-197
4	123	43.2	443	7	US-11-272-833-4
5	123	43.2	463	6	US-10-131-826A-360
6	123	43.2	463	6	US-10-973-115B-262
7	123	43.2	463	7	US-11-154-673-9
8	123	43.2	463	7	US-11-290-153-360
9	123	43.2	506	7	US-11-154-673-2
10	123	43.2	550	7	US-11-154-673-8
11	123	43.2	593	7	US-11-154-673-3
12	123	43.2	625	7	US-11-154-673-7
13	116	40.7	258	7	US-11-090-439-38
14	111.5	39.1	245	6	US-10-515-868-6
15	111	38.9	383	6	US-10-453-372-88
16	111	38.9	457	6	US-10-453-372-84
17	111	38.9	475	6	US-10-453-372-98
18	111	38.9	477	6	US-10-453-372-90
19	111	38.9	497	6	US-10-453-372-92
20	111	38.9	497	6	US-10-453-372-100
21	111	38.9	497	6	US-10-453-372-102
22	111	38.9	497	6	US-10-218-784-56
23	111	38.9	497	6	US-10-219-061-56
24	111	38.9	497	6	US-10-219-062-56
25	111	38.9	497	6	US-10-219-064-56

26	111	38.9	497	6	US-10-233-134-56	Sequence 56, Appl
27	111	38.9	498	6	US-10-453-372-94	Sequence 94, Appl
28	109	38.2	243	6	US-10-515-868-4	Sequence 4, Appl
29	109	38.2	243	6	US-10-506-443A-41	Sequence 41, Appl
30	108.5	38.1	242	6	US-10-131-826A-262	Sequence 262, App
31	108.5	38.1	242	6	US-10-973-115B-262	Sequence 262, App
32	108.5	38.1	242	7	US-11-290-153-262	Sequence 262, App
33	106	37.2	500	6	US-10-194-487-70	Sequence 70, Appl
34	106	37.2	500	6	US-10-195-883-70	Sequence 70, Appl
35	106	37.2	500	6	US-10-195-888-70	Sequence 70, Appl
36	106	37.2	500	6	US-10-195-889-70	Sequence 70, Appl
37	106	37.2	500	7	US-11-067-573-2	Sequence 2, Appl
38	99.5	34.9	190	7	US-11-031-206-90	Sequence 90, Appl
39	98.5	34.6	216	7	US-11-038-285A-9	Sequence 9, Appl
40	98.5	34.6	219	7	US-11-272-833-7	Sequence 7, Appl
41	98.5	34.6	220	7	US-11-153-222A-3	Sequence 3, Appl
42	98.5	34.6	221	7	US-11-038-285A-11	Sequence 11, Appl
43	98.5	34.6	231	7	US-11-038-285A-10	Sequence 10, Appl
44	98.5	34.6	265	7	US-11-038-285A-7	Sequence 7, Appl
45	98.5	34.6	266	7	US-11-038-285A-5	Sequence 5, Appl

ALIGNMENTS

RESULT 1
US-10-498-026-76
; Sequence 76, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 76
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-76

Query Match 97.9%; Score 279; DB 6; Length 227;
Best Local Similarity 98.0%; Pred. No. 5.8e-29;
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 HYTMWANTKEVCGSGSIKYIQEKWHKHYLCVNYGSPGNFKNEELYQTK 49
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Db 179 HYTMWANTKEVCGSGSIKYIQEKWHKHYLCVNYGSPGNFKNEELYQTK 227

RESULT 2
US-10-498-026-80
; Sequence 80, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 80
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-80

Query Match 83.2%; Score 237; DB 6; Length 206;
Best Local Similarity 73.5%; Pred. No. 1.6e-23;
Matches 36; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

ORGANISM: Vespula vulgaris
US-10-091-135-16

Query Match 100.0%; Score 285; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 1e-28; Indels 0; Gaps 0;
Matches 49; Conservative 0; Mismatches 0;

QY 1 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 49
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DB 156 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 204
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RESULT 3

US-10-719-553-39
Sequence 39, Application US/10719553
Publication No. US20040091500A1
GENERAL INFORMATION:
APPLICANT: Ipsen, Hans Henrik
APPLICANT: Spangfort, Michael Dho
APPLICANT: Larsen Jorgen Nedergaard
TITLE OF INVENTION: NOVEL RECOMBINANT ALLERGENS
FILE REFERENCE: 04305/100E144-US2
CURRENT APPLICATION NUMBER: US/10/719,553
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 09/270,910
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/078,371
PRIOR FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 39
LENGTH: 204
TYPE: PRT
ORGANISM: vespula vulgaris
US-10-719-553-39

Query Match 100.0%; Score 285; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 1e-28; Indels 0; Gaps 0;
Matches 49; Conservative 0; Mismatches 0;

QY 1 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 49
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DB 156 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 204
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RESULT 4

US-09-957-806A-22
Sequence 22, Application US/09957806A
Publication No. US20050181446A1
GENERAL INFORMATION:
APPLICANT: Roggen, Erwin
APPLICANT: Ernst, Steffen
APPLICANT: Svendsen, Allan
APPLICANT: Friis, Eeben
APPLICANT: Osten, Claus
TITLE OF INVENTION: PROTEIN VARIANTS HAVING MODIFIED IMMUNOGENICITY
FILE REFERENCE: 10021.204-US
CURRENT APPLICATION NUMBER: US/09/957,806A
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 248
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 209
TYPE: PRT
ORGANISM: Vespula vulgaris
US-09-957-806A-22

Query Match 100.0%; Score 285; DB 3; Length 209;
Best Local Similarity 100.0%; Pred. No. 1.1e-28; Indels 0; Gaps 0;
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DB 161 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 209
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RESULT 5

US-10-001-245-214
Sequence 214, Application US/10001245
Publication No. US20030175312A1
GENERAL INFORMATION:
APPLICANT: HOLM, Jens
APPLICANT: IPSSEN, Henrik
APPLICANT: LARSEN, Jorgen N.
APPLICANT: SPANGFORT, Michael D.
TITLE OF INVENTION: No. US20030175312A1el mutant allergens
FILE REFERENCE: 4305/1H942-US2
CURRENT APPLICATION NUMBER: US/10/001,245
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/298,170
PRIOR FILING DATE: 2001-06-14
PRIOR APPLICATION NUMBER: US 60/249,361
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 217
SOFTWARE: PatentIn version 3.1
SEQ ID NO 214
LENGTH: 210
TYPE: PRT
ORGANISM: Vespula vulgaris
NAME/KEY: MISC FEATURE
LOCATION: (1)-(210)
OTHER INFORMATION: where X is any amino acid
US-10-001-245-214

Query Match 100.0%; Score 285; DB 4; Length 210;
Best Local Similarity 100.0%; Pred. No. 1.1e-28; Indels 0; Gaps 0;
Matches 49; Conservative 0; Mismatches 0;

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DB 162 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 210
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RESULT 6

US-10-091-135-64
Sequence 64, Application US/10091135
Publication No. US20030039660A1
GENERAL INFORMATION:
APPLICANT: King, Te Piao
APPLICANT: Spangfort, Michael Dho
TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN
FILE REFERENCE: 2313/1H587-US1
CURRENT APPLICATION NUMBER: US/10/091,135
CURRENT FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: US 60/272,818
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn version 3.1
SEQ ID NO 64
LENGTH: 204
TYPE: PRT
ORGANISM: Vespula vulgaris
US-10-091-135-64

Query Match 97.9%; Score 279; DB 4; Length 204;
Best Local Similarity 98.0%; Pred. No. 6.3e-28; Indels 0; Gaps 0;
Matches 48; Conservative 0; Mismatches 1;

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DB 156 HYTMVWANTKEVCGSIIKIQEKWHKHYLVNCGPSGNFKNEELYQTK 204
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RESULT 7

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:05:57 ; Search time 74.9962 Seconds
(without alignments) 272.996 Million cell updates/sec

Title: US-10-091-135-8
 Perfect score: 285
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Total number of hits satisfying chosen parameters: 1867569

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Maximum DB seq length: 2000000000
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Post-processing: Minimum Match 0%
Maximum Match 100%
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	285	100.0	204	4	US-10-719-553-39		Sequence 39, Appl
4	285	100.0	209	3	US-09-957-8064-22		Sequence 22, Appl
5	285	100.0	210	4	US-10-001-245-214		Sequence 214, App
6	279	97.9	204	4	US-10-091-135-64		Sequence 64, Appl
7	279	97.9	204	4	US-10-091-135-81		Sequence 81, Appl
8	279	97.9	227	3	US-09-847-208-170		Sequence 170, App
9	279	97.9	227	5	US-10-809-689-82		Sequence 82, Appl
10	277	97.2	204	3	US-09-847-208-162		Sequence 162, App
11	277	97.2	204	4	US-10-091-135-65		Sequence 65, Appl
12	276	96.8	204	3	US-09-847-208-165		Sequence 165, App
13	276	96.8	204	4	US-10-091-135-63		Sequence 63, Appl
14	275	96.5	204	3	US-09-847-208-163		Sequence 163, App
15	275	96.5	204	4	US-10-091-135-67		Sequence 67, Appl
16	271	95.1	203	4	US-10-001-245-118		Sequence 118, App
17	268	94.0	204	3	US-09-847-208-166		Sequence 166, App
18	268	94.0	204	4	US-10-091-135-66		Sequence 66, Appl
19	255.5	89.6	198	4	US-10-001-245-121		Sequence 121, App
20	255.5	89.6	202	4	US-10-001-245-117		Sequence 117, App
21	251.5	88.2	201	4	US-10-001-245-119		Sequence 119, App
22	249.5	87.5	192	4	US-10-001-245-122		Sequence 122, App
23	240	84.2	194	4	US-10-001-245-120		Sequence 120, App
24	237	83.2	206	3	US-09-847-208-171		Sequence 171, App
25	237	83.2	206	4	US-10-091-135-68		Sequence 68, Appl
26	237	83.2	206	5	US-10-809-689-86		Sequence 86, Appl
27	227	79.6	202	3	US-09-847-208-172		Sequence 172, App

28	227	79.6	202	4	US-10-091-135-73	Sequence 73, App
29	226	79.3	202	3	US-09-847-208-160	Sequence 160, App
30	226	79.3	202	4	US-10-091-135-74	Sequence 74, App
31	226	79.3	203	3	US-09-847-208-86	Sequence 86, App
32	226	79.3	203	4	US-10-091-135-71	Sequence 71, App
33	226	79.3	203	3	US-09-847-208-167	Sequence 167, App
34	225	78.9	205	4	US-10-091-135-69	Sequence 69, App
35	217	76.1	205	4	US-10-091-135-72	Sequence 72, App
36	217	76.1	215	3	US-09-847-208-91	Sequence 91, App
37	215	75.4	202	3	US-09-847-208-161	Sequence 161, App
38	215	75.4	202	4	US-10-091-135-75	Sequence 75, App
39	210	73.7	204	4	US-10-091-135-70	Sequence 70, App
40	210	73.7	227	3	US-09-847-208-90	Sequence 90, App
41	195	68.4	206	3	US-09-847-208-150	Sequence 150, App
42	189	66.3	203	3	US-09-847-208-151	Sequence 151, App
43	189	66.3	205	4	US-10-091-135-77	Sequence 77, App
44	187	65.6	211	3	US-09-847-208-159	Sequence 159, App
45	187	65.6	211	4	US-10-091-135-80	Sequence 80, App

ALIGNMENTS

RESULT 1
 US-10-091-135-8
 ; Sequence 8, Application US/10091135
 ; Publication No. US2003003960A1
 ; GENERAL INFORMATION:
 ; APPLICANT: King, Te Piao
 ; APPLICANT: Spangfort, Michael Dho
 ; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
 ; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN
 ; FILE REFERENCE: 2313/1HS87-US1
 ; CURRENT APPLICATION NUMBER: US/10/091.135
 ; CURRENT FILING DATE: 2002-03-04
 ; PRIOR APPLICATION NUMBER: US 60/272,818
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 98
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO 8
 ; LENGTH: 49
 ; TYPE: PRT
 ; ORGANISM: *Vespula vulgaris*
 ; US-10-091-135-8

Query Match	100.0%;	Score 285;	DB 4;	Length 49;
Best Local Similarity	100.0%;	Pred. No. 2.2e-29;		
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	1	HYDTMYWANKYVCGSGIKYIQEKWKHGYLVCMVPGSGNFKNIELYQTK	49	

RESULT 2
 US-10-091-135-16
 ; Sequence 16, Application US/10091135
 ; Publication No. US20030039660A1
 ;
 ; GENERAL INFORMATION:
 ;
 ; APPLICANT: King, Te Piao
 ; APPLICANT: Spangfort, Michael Dho
 ;
 ; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
 ; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGENS
 ;
 ; FILE REFERENCE: 2313/1H587-US1
 ; CURRENT APPLICATION NUMBER: US/10/091,135
 ; CURRENT FILING DATE: 2002-03-04
 ; PRIOR APPLICATION NUMBER: US 60/272,818
 ; PRIOR FILING DATE: 2001-03-02
 ; NUMBER OF SEQ ID NOS: 98
 ; SOFTWARE: PatentIn version 3.1
 ;
 ; SEQ ID NO 16
 ; LENGTH: 204
 ; TYPE: PRT

QY 1 HYTMVWANTKEVCGSIKIYQEKWHKHYLVNCGPSGNFKNEELYQTK 49
156 HYTMVWANTKEVCGSIKIYQEKWHKHYLVNCGPSGNFKNEELYQTK 204
Db

RESULT 2

US-08-614-935-2
Sequence 2, Application US/08614935
Patent No. 5804201
GENERAL INFORMATION:
APPLICANT: King, Te P.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Vesputia vulgaris

US-08-614-935-2
Query Match 97.9%; Score 279; DB 1; Length 204;
Best Local Similarity 98.0%; Pred. No. 7.4e-30;
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYTMVWANTKEVCGSIKIYQEKWHKHYLVNCGPSGNFKNEELYQTK 49
156 HYTMVWANTKEVCGSIKIYQEKWHKHYLVNCGPSGNFKNEELYQTK 204
Db

RESULT 3

US-09-130-287-2
Sequence 2, Application US/09130287
Patent No. 6106844
GENERAL INFORMATION:
APPLICANT: King, Te P.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,287
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-156 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Vesputia vulgaris

US-09-130-287-2
Query Match 97.9%; Score 279; DB 2; Length 204;
Best Local Similarity 98.0%; Pred. No. 7.4e-30;
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYTMVWANTKEVCGSIKIYQEKWHKHYLVNCGPSGNFKNEELYQTK 49
156 HYTMVWANTKEVCGSIKIYQEKWHKHYLVNCGPSGNFKNEELYQTK 204
Db

RESULT 4

US-09-541-759-6
Sequence 6, Application US/09541759
Patent No. 6723322
GENERAL INFORMATION:
APPLICANT: Lustigman, Sara
APPLICANT: Pearlman, Eric
APPLICANT: Unnasch, Thomas
TITLE OF INVENTION: ANGIOGENIC ONCHOCERCA VOLVULUS PROTEINS AND USES THEREOF
FILE REFERENCE: 63475/252
CURRENT APPLICATION NUMBER: US/09/541,759
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patent In version 3.0
SEQ ID NO 6
LENGTH: 227
TYPE: PRT
ORGANISM: Vesputia vulgaris
US-09-541-759-6

Query Match 97.9%; Score 279; DB 2; Length 227;
Best Local Similarity 98.0%; Pred. No. 8.4e-30;
Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2006, 10:57:41 ; Search time 14.7748 Seconds
(without alignments)
274.190 Million cell updates/sec

Title: US-10-091-135-8
Perfect score: 285
Sequence: 1 HVTQWVWANTKEVGGSIKY.....LVCNYGPGSNFKNEELYQTK 49

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
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2: /cgn2_6/ptodata/1/1aa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/H COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/ECTUS COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	279	97.9	204	1	US-08-419-414-9
2	279	97.9	204	1	US-08-614-935-2
3	279	97.9	204	2	US-09-130-287-2
4	279	97.9	227	2	US-09-541-759-6
5	276	96.8	204	1	US-08-614-935-1
6	276	96.8	204	2	US-09-130-287-1
7	226	79.3	203	1	US-08-419-414-8
8	226	79.3	203	1	US-08-614-935-3
9	226	79.3	203	2	US-09-130-287-3
10	217	76.1	205	1	US-08-614-935-4
11	217	76.1	205	2	US-09-130-287-4
12	210	73.7	166	1	US-08-614-935-30
13	210	73.7	166	2	US-09-130-287-30
14	210	73.7	204	1	US-08-614-935-5
15	210	73.7	204	2	US-09-130-287-5
16	203	71.2	125	1	US-07-857-224B-114
17	196	68.8	124	1	US-07-857-224B-113
18	189	66.3	205	1	US-08-614-935-7
19	189	66.3	205	2	US-09-130-287-7
20	181	63.5	205	1	US-08-419-414-10
21	181	63.5	205	1	US-08-614-935-6
22	181	63.5	205	2	US-09-130-287-6
23	123	43.2	20	1	US-08-614-935-76
24	123	43.2	20	2	US-09-130-287-76
25	123	43.2	270	1	US-08-773-368-1
26	123	43.2	270	2	US-09-199-887-1
27	123	43.2	463	2	US-09-907-794A-285

ALIGNMENTS

RESULT 1

US-08-419-414-9

; Sequence 9, Application US/08419414

; Patent No. 5753787

; GENERAL INFORMATION:

; APPLICANT: Hawdon, John M.

; APPLICANT: Hotez, Peter J.

; APPLICANT: Jones, Brian F.

; TITLE OF INVENTION: Hookworm Vaccine

; NUMBER OF SEQUENCES: 16

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patrea L. Pabst

; STREET: 2800 One Atlantic Center

; STREET: 1201 West Peachtree Street

; CITY: Atlanta

; STATE: Georgia

; COUNTRY: USA

; ZIP: 30309-3450

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/419,414

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Pabst, Patrea L.

; REGISTRATION NUMBER: 31,284

; REFERENCE/DOCKET NUMBER: YU113

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (404) 873-8795

; TELEFAX: (404) 873-8795

; INFORMATION FOR SEQ ID NO: 9:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 204 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; HYPOTHETICAL: NO

; ANTI-SENSE: NO

; ORIGINAL SOURCE:

; ORGANISM: Vespula vulgaris

US-08-419-414-9

Query Match 97.9%; Score 279; DB 1; Length 204;

Best Local Similarity 98.0%; Pred. No. 7.4e-30;

Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

FT DISULFID 31 124 By similarity.
 FT DISULFID 49 117 By similarity.
 FT DISULFID 193 210 By similarity.
 FT CONFLICT 109 109 V -> I (in Ref. 2).
 FT CONFLICT 118 118 Q -> E (in Ref. 2).
 FT CONFLICT 173 173 D -> N (in Ref. 2).
 FT CONFLICT 219 219 M -> K (in Ref. 2).
 FT HELIX 26 28
 FT TURN 32 33
 FT TURN 38 41
 FT HELIX 53 57
 FT STRAND 61 79
 FT TURN 80 81
 FT TURN 87 88
 FT TURN 94 94
 FT STRAND 101 102
 FT HELIX 104 114
 FT TURN 115 116
 FT STRAND 133 141
 FT HELIX 149 157
 FT HELIX 158 162
 FT TURN 165 166
 FT HELIX 169 171
 FT HELIX 174 183
 FT TURN 184 184
 FT TURN 186 187
 FT TURN 190 200
 FT TURN 201 202
 FT STRAND 203 213
 FT TURN 219 220
 FT TURN 226 227
 SQ SEQUENCE 227 AA; 99E9813740A66F55 CRC64;
 Query Match 97.9%; Score 279; DB 1; Length 227;
 Best Local Similarity 98.0%; Pred. No. 1.3e-27;
 Matches 48; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 HYTMWANTKEVCGSGIKYIQEKWKHYLVNCGPSGNFQNEELYQTK 49
 DB 179 HYTMWANTKEVCGSGIKYIQEKWKHYLVNCGPSGNFQNEELYQTK 227
 RESULT 2
 VA5 VESFL STANDARD; PRT; 204 AA.
 ID VA5 VESFL
 AC P35783; 1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Venom allergen 5 (Antigen 5) (Ags) (Allergen Ves f 5) (Ves f V).
 OS Vesputia flavopilosa (Yellow jacket) (Wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vesputidae; Vespinae; Vespula.
 OX NCBI_TaxID=30211;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=94044316; PubMed=8227862;
 RA Hoffman D.R.;
 RT "Allergens in Hymenoptera venom. XXV: the amino acid sequences of antigen 5 molecules and the structural basis of antigenic cross-reactivity".
 RL J. Allergy Clin. Immunol. 92:707-716(1993).
 CC -1- FUNCTION: May have an ancestral function in the promotion of ovum fertilization by sperm.
 CC -1- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
 CC -1- ALLERGEN: Causes an allergic reaction in human.
 CC -1- SIMILARITY: Belongs to the CRISP family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 PIR; B37329; B37329.
 DR HSSP; Q05110; IQNX.
 SMR; P35760; 1-204.
 DR InterPro; IPR001283; Allrgn_V5/Tpx1.
 DR InterPro; IPR002413; V5_allergen.
 DR Pfam; PF00188; SCP; 1.
 DR PRINTS; PR00837; V5TPXLIKE.
 DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
 DR SMART; SM00198; SCP; 1.
 DR PROSITE; PS01009; CRISP_1; 1.
 DR PROSITE; PS01010; CRISP_2; 1.
 KW Allergen; Direct protein sequencing.
 FT DISULFID 4 17 By similarity.
 FT DISULFID 8 101 By similarity.
 FT DISULFID 26 94 By similarity.
 FT DISULFID 170 187 By similarity.
 SQ SEQUENCE 204 AA; 23274 MW; 7667232536AB2FC5 CRC64;
 Query Match 97.2%; Score 277; DB 1; Length 204;
 Best Local Similarity 95.9%; Pred. No. 2.1e-27;
 Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYTMWANTKEVCGSGIKYIQEKWKHYLVNCGPSGNFQNEELYQTK 49
 DB 156 HYTMWANTKEVCGSGIKYIQEKWKHYLVNCGPSGNFQNEELYQTK 204
 RESULT 3
 VA5 VESMC STANDARD; PRT; 204 AA.
 ID VA5 VESMC
 AC P35760;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Venom allergen 5 (Antigen 5) (Ags) (Allergen Ves m 5) (Ves m V).
 OS Vesputia maculifrons (Eastern yellow jacket) (Wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vesputidae; Vespinae; Vespula.
 OX NCBI_TaxID=7453;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=93203603; PubMed=8454859;
 RA Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
 RT "Sequence analysis and antigenic cross-reactivity of a venom allergen, antigen 5, from hornets, wasps, and yellow jackets".
 RL J. Immunol. 150:2823-2830(1993).
 CC -1- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
 CC -1- ALLERGEN: Causes an allergic reaction in human.
 CC -1- SIMILARITY: Belongs to the CRISP family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 PIR; B37329; B37329.
 DR HSSP; Q05110; IQNX.
 SMR; P35760; 1-204.
 DR InterPro; IPR001283; Allrgn_V5/Tpx1.
 DR InterPro; IPR002413; V5_allergen.
 DR Pfam; PF00188; SCP; 1.
 DR PRINTS; PR00837; V5TPXLIKE.
 DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
 DR SMART; SM00198; SCP; 1.
 DR PROSITE; PS01009; CRISP_1; 1.

CC use as long as its content is in no way modified and this statement is not removed.
 CC PIR; A44583; A44583.
 DR HSSP; Q05110; IQNX.
 SMR; P35783; 1-204.
 DR InterPro; IPR001283; Allrgn_V5/Tpx1.
 DR InterPro; IPR002413; V5_allergen.
 DR Pfam; PF00188; SCP; 1.
 DR PRINTS; PR00837; V5TPXLIKE.
 DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
 DR SMART; SM00198; SCP; 1.
 DR PROSITE; PS01009; CRISP_1; 1.
 DR PROSITE; PS01010; CRISP_2; 1.
 KW Allergen; Direct protein sequencing.
 FT DISULFID 4 17 By similarity.
 FT DISULFID 8 101 By similarity.
 FT DISULFID 26 94 By similarity.
 FT DISULFID 170 187 By similarity.
 SQ SEQUENCE 204 AA; 23274 MW; 7667232536AB2FC5 CRC64;
 Query Match 97.2%; Score 277; DB 1; Length 204;
 Best Local Similarity 95.9%; Pred. No. 2.1e-27;
 Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 HYTMWANTKEVCGSGIKYIQEKWKHYLVNCGPSGNFQNEELYQTK 49
 DB 156 HYTMWANTKEVCGSGIKYIQEKWKHYLVNCGPSGNFQNEELYQTK 204
 RESULT 3
 VA5 VESMC STANDARD; PRT; 204 AA.
 ID VA5 VESMC
 AC P35760;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Venom allergen 5 (Antigen 5) (Ags) (Allergen Ves m 5) (Ves m V).
 OS Vesputia maculifrons (Eastern yellow jacket) (Wasp).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vesputidae; Vespinae; Vespula.
 OX NCBI_TaxID=7453;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Venom;
 RX MEDLINE=93203603; PubMed=8454859;
 RA Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
 RT "Sequence analysis and antigenic cross-reactivity of a venom allergen, antigen 5, from hornets, wasps, and yellow jackets".
 RL J. Immunol. 150:2823-2830(1993).
 CC -1- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
 CC -1- ALLERGEN: Causes an allergic reaction in human.
 CC -1- SIMILARITY: Belongs to the CRISP family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation at the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 PIR; B37329; B37329.
 DR HSSP; Q05110; IQNX.
 SMR; P35760; 1-204.
 DR InterPro; IPR001283; Allrgn_V5/Tpx1.
 DR InterPro; IPR002413; V5_allergen.
 DR Pfam; PF00188; SCP; 1.
 DR PRINTS; PR00837; V5TPXLIKE.
 DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.
 DR SMART; SM00198; SCP; 1.
 DR PROSITE; PS01009; CRISP_1; 1.

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2006, 10:53:37 ; Search time 72.3779 Seconds
(without alignments)
477.644 Million cell updates/sec

Title: US-10-091-135-8
Perfect score: 285
Sequence: 1 HYQMWANTKEVCGSIKY.....LVCNYGSPGNKNEELYQTK 49

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	279	97.9	227	1 VA5 VESVU	Q05110 vespula vul
2	277	97.2	204	1 VA5 VESFL	P35783 vespula fla
3	276	96.8	204	1 VA5 VESMC	P35760 vespula mac
4	275	96.5	204	1 VA5 VESGE	P35784 vespula ger
5	268	94.0	204	1 VA5 VESPE	P35785 vespula pen
6	237	83.2	206	1 VA5 VESVI	P35787 vespula vid
7	227	79.6	202	1 VA5 VESMA	P81657 vespa manda
8	226	79.3	202	1 VA51 VESCR	P35781 vespa crabr
9	226	79.3	203	1 VA5 DOLAR	Q05108 dolichovesp
10	225	78.9	205	1 VA5 VESSQ	P35786 vespula equ
11	217	76.1	215	1 VA53 DOLMA	P10737 dolichovesp
12	215	75.4	202	1 VA52 VESCR	P35782 vespa crabr
13	210	73.7	227	1 VA52 DOLMA	P10736 dolichovesp
14	195	68.4	206	1 VA5 BOLDQ	P81656 polistes do
15	195	68.4	227	2 Q88KJ8 POLDO	Q88KJ8 polistes do
16	194	68.1	207	1 VA5 POLGA	P83377 polistes ga
17	194	68.1	207	1 VA5 POLSR	Q72156 polybia scu
18	189	66.3	205	1 VA5 POLEX	P35779 solenopsis ex
19	187	65.6	211	1 VA3 SOLRI	P35779 solenopsis ex
20	182.5	64.0	226	2 Q88KJ9 POLEX	Q88KJ9 polistes ex
21	182	63.9	205	1 VA5 POLFU	P35780 polistes fu
22	181	63.5	209	1 VA5 POLAN	Q05109 polistes an
23	164.5	57.7	234	1 VA3 SOLIN	P35778 solenopsis
24	132	46.3	464	2 Q58D34 BOVIN	Q58D34 bos taurus
25	129.5	45.4	250	2 Q7YSZ5 RHOPR	Q7YSZ5 rhodnius pr
26	127	44.6	474	2 Q8CHU4 MOUSE	Q8CHU4 mus musculu
27	127	44.6	489	2 Q8ET66 MOUSE	Q8ET66 mus musculu
28	127	44.6	489	2 Q9UJ5C MOUSE	Q9UJ5C mus musculu
29	123	43.2	270	2 Q6ZVG5 HUMAN	Q6ZVG5 homo sapien
30	123	43.2	408	2 Q8TCB8 HUMAN	Q8TCB8 homo sapien
31	123	43.2	428	2 Q8IYL8 HUMAN	Q8IYL8 homo sapien

32	123	43.2	463	2	Q6UXB8 HUMAN	Q6UXB8 homo sapien
33	123	43.2	463	2	Q8NBK0 HUMAN	Q8NBK0 homo sapien
34	122.5	43.0	363	2	Q5DA03 SCHJA	Q5DA03 schistosoma
35	122	42.8	881	1	PRY3 YEAST	P47033 saccharomyc
36	121	42.5	210	2	Q7Z1H1 NECAM	Q7Z1H1 necator ame
37	120	42.1	188	2	Q9Z0U6 RAT	Q9Z0U6 rattus norv
38	120	42.1	246	2	Q60ZV8 CAEBR	Q60ZV8 caenorhabdi
39	120	42.1	246	2	P90958 CAESL	P90958 caenorhabdi
40	120	42.1	429	2	Q614N2 CAEBR	Q614N2 caenorhabdi
41	119	41.8	494	2	Q9D2R3 MOUSE	Q9D2R3 mus musculu
42	119	41.8	495	2	Q8BZQ2 MOUSE	Q8BZQ2 mus musculu
43	118	41.4	253	2	Q9H3Y0 HUMAN	Q9H3Y0 homo sapien
44	118	41.4	504	2	Q69HL7 CIOIN	Q69HL7 ciona intes
45	116	40.7	258	2	Q43692 HUMAN	Q43692 homo sapien

ALIGNMENTS

RESULT 1

VA5 VESVU

ID VA5 VESVU STANDARD; PRT; 227 AA.

AC Q05110; Q9UB91;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Venom allergen 5 precursor (Antigen 5) (Ags) (Allergen Ves v 5) (Ves v

DE Venom allergen 5 precursor (Antigen 5) (Ags) (Allergen Ves v 5) (Ves v

DE Venom allergen 5 precursor (Antigen 5) (Ags) (Allergen Ves v 5) (Ves v

OS Vespula vulgaris (Yellow jacket) (Wasp).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;

OC Vespidae; Vespinae; Vespula.

OX NCBI_TaxID=7454;

RN [1]

RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.

RC TISSUE=Venom;

FX MEDLINE=93203603; PubMed=8454859;

RA Lu G., Vallalaba M., Coscia M.R., Hoffman D.R., King T.P.;

RT "Sequence analysis and antigenic cross-reactivity of a venom allergen,

RT antigen 5, from hornets, wasps, and yellow jackets.";

RL J. Immunol. 150:2823-2830(1993).

RN [2]

RP NUCLEOTIDE SEQUENCE OF 24-227.

Suck R., Hagen S., Fiebig H.;

RA "Molecular cloning of a genomic sequence from the venom allergen

RT antigen 5 from Vespula vulgaris.";

RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoir.

CC -!- ALLERGEN: Causes an allergic reaction in human.

CC -!- SIMILARITY: Belongs to the CRISP family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use as long as its content is in no way modified and this statement is not

CC removed.

CC EMBL; M98858; AAA30333.1; -; mRNA.

DR EMBL; AJ238849; CAB22897.1; -; Genomic_DNA.

DR FDB; 1ONX; X-ray; A=24-227.

DR InterPro; IPR001283; Allrgn_V5/Tpx1.

DR InterPro; IPR002413; V5_allergen.

DR Pfam; PF00188; SCP; 1.

DR PRINTS; PR00838; VSALLERGEN.

DR PRINTS; PR00837; VSTPXLKE.

DR PRODOM; PD000542; Allrgn_V5/Tpx1; 1.

DR SMART; SM00198; SCP; 1.

DR	PROSITE; PS01009; CRISP 1; 1.					
DR	PROSITE; PS01010; CRISP 2; 1.					
KW	3D-structure; Allergen; Direct protein sequencing; Signal.					
FT	SIGNAL	1	23			
FT	CHAIN	24	227			Venom allergen 5.
FT	DISULFID	27	40			By similarity.

B44583
venom allergen antigen Ves g 5 - German yellowjacket
C;Species: Vespula germanica (German yellowjacket)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: B44583; A44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 molecul
A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: B44583
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-204 <HOF>
A;Cross-references: UNIPROT:P35784; UNIPARC:UPI0000138090
C;Superfamily: yellowjacket venom allergen antigen 5

Query Match 96.5%; Score 275; DB 2; Length 204;
Best Local Similarity 95.9%; Pred. No. 5.1e-27;
Matches 47; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYTQMWWANTKEVCGSGIKYIQEKWHKHLYVCNYGPSGNFKNEELYQTK 49
|||||
DB 156 HYTQMWWANTKEVCGSGIKYIQDKWHKHLYVCNYGPSGNFKNEELYQTK 204
|||||

RESULT 4
C44583
venom allergen antigen Ves p 5 - western yellowjacket
C;Species: Vespula pensylvanica (western yellowjacket)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: C44583; C44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 molecul
A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: C44583
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-204 <HOF>
A;Cross-references: UNIPROT:P35785; UNIPARC:UPI0000138093
C;Superfamily: yellowjacket venom allergen antigen 5

Query Match 94.0%; Score 268; DB 2; Length 204;
Best Local Similarity 93.8%; Pred. No. 3.9e-26;
Matches 45; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 HYTQMWWANTKEVCGSGIKYIQEKWHKHLYVCNYGPSGNFKNEELYQTK 49
|||||
DB 156 HYTQMWWANTKEVCGSGIKYIQENWHKHLYVCNYGPSGNFKNEELYQTK 204
|||||

RESULT 5
E44583
venom allergen antigen Ves vi 5 - yellowjacket (Vespula vidua)
C;Species: Vespula vidua
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: E44583; E44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 molecul
A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: E44583
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-206 <HOF>
A;Cross-references: UNIPROT:P35787; UNIPARC:UPI0000138095
C;Superfamily: yellowjacket venom allergen antigen 5

Query Match 83.2%; Score 237; DB 2; Length 206;
Best Local Similarity 73.5%; Pred. No. 3e-22;
Matches 36; Conservative 10; Mismatches 3; Indels 0; Gaps 0;

QY 1 HYTQMWWANTKEVCGSGIKYIQEKWHKHLYVCNYGPSGNFKNEELYQTK 49

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:56:21 ; Search time 10.2863 Seconds
(without alignments)
458.342 Million cell updates/sec

Title: US-10-091-135-8
Perfect score: 285
Sequence: 1 HYTQWVWANTKEVGGSIKY.....LVCNYGPGSNFKNELYQTK 49

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80: *
1: Pir1: *
2: Pir2: *
3: Pir3: *
4: Pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	277	97.2	204	2 A44583	venom allergen ant
2	276	96.8	204	2 B37329	antigen 5 - easter
3	275	96.5	204	2 B44583	venom allergen ant
4	268	94.0	204	2 C44583	venom allergen ant
5	237	83.2	206	2 E44583	venom allergen ant
6	226	79.3	202	2 G44583	venom allergen ant
7	225	78.9	205	2 D44583	venom allergen ant
8	215	75.4	202	2 H44583	venom allergen ant
9	213	74.7	213	2 B31085	antigen 5-3 precu
10	210	73.7	227	2 A31085	antigen 5-2 precu
11	189	66.3	205	2 A37329	antigen 5 - paper
12	187	65.6	211	2 B58853	venom allergen Sol
13	182	63.9	205	2 F44583	venom allergen ant
14	159.5	56.0	212	2 B37330	venom allergen III
15	122	42.8	881	2 S56032	probable membrane
16	120	42.1	246	2 T24493	hypothetical prote
17	116	40.7	425	2 C89753	protein FilC7.3 fi
18	113	39.6	173	2 S4171	Gene PR-1 protein
19	112	39.3	299	2 S56031	pathogenesis-relat
20	111.5	39.1	167	2 S51679	pathogenesis-relat
21	111.5	39.1	245	2 S68691	neutrophil granule
22	109	38.2	243	2 B33329	cysteine-rich secr
23	108.5	38.1	212	2 T22437	hypothetical prote
24	107	37.5	161	2 E85354	PR-1-like protein
25	106.5	37.4	179	2 S23531	pathogenesis-relat
26	106.5	37.4	312	2 T16415	hypothetical prote
27	106	37.2	262	2 T24854	hypothetical prote
28	105.5	37.0	159	2 S26238	pathogenesis-relat
29	105	36.8	210	2 T04233	pathogenesis-relat

30	102.5	36.0	168	2 A24620	pathogenesis-relat
31	102.5	36.0	177	2 T08126	pathogenesis-relat
32	101.5	35.6	159	1 VCT014	pathogenesis-relat
33	101.5	35.6	207	2 T22438	hypothetical prote
34	101	35.4	208	2 T19852	hypothetical prote
35	100.5	35.3	184	2 S10205	pathogenesis-relat
36	99.5	34.9	177	2 S04728	pathogenesis-relat
37	99.5	34.9	190	2 T04232	pathogenesis-relat
38	99	34.7	208	2 T20661	hypothetical prote
39	99	34.7	329	2 S38082	pathogenesis-relat
40	98.5	34.6	163	2 T04989	pathogenesis-relat
41	98.5	34.6	219	2 JC4131	glioma pathogenesi
42	98.5	34.6	266	2 JC5308	testis-specific, v
43	98	34.4	205	2 T48294	pathogenesis relat
44	98	34.4	207	2 T22436	hypothetical prote
45	97	34.0	176	2 F04583	pathogenesis-relat

ALIGNMENTS

RESULT 1

A44583
venom allergen antigen Ves f 5 - yellowjacket (Vespula flavopilosa)
C:Species: Vespula flavopilosa
C>Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A44583; B44522
R:Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mol.
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: A44583
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
A:Cross-references: UNIPROT:P35783; UNIPARC:UPI000013808F
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 97.2%; Score 277; DB 2; Length 204;
Best Local Similarity 95.9%; Pred. No. 2.9e-27;
Matches 47; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTQWVWANTKEVGGSIKYIOEKWHKHYLCVNYGPGSNFKNELYQTK 49
|||||
Db 156 HYTQWVWANTKEVGGSIKFIQEKWHKHYLCVNYGPGSNFQNEELYQTK 204

RESULT 2

B37329
antigen 5 - eastern yellowjacket
C:Species: Vespula maculifrons (eastern yellowjacket)
C>Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C:Accession: B37329
R:Lu, G.; Villalba, M.; Coscia, M.R.; Hoffman, D.R.; King, T.P.
Submitted to the Protein Sequence Database, August 1992
A:Reference number: A37329
A:Accession: B37329
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <LUI>
A:Cross-references: UNIPROT:P35760; UNIPARC:UPI0000138092
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 96.8%; Score 276; DB 2; Length 204;
Best Local Similarity 95.9%; Pred. No. 3.9e-27;
Matches 47; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 HYTQWVWANTKEVGGSIKYIOEKWHKHYLCVNYGPGSNFKNELYQTK 49
|||||
Db 156 HYTQWVWANTKEVGGSIKFIQEKWHKHYLCVNYGPGSNFQNEELYQTK 204

RESULT 3

XX SQ Sequence 49 AA; Query Match 100.0%; Score 285; DB 5; Length 49;
 Best Local Similarity 100.0%; Pred. No. 5.3e-32; Mismatches 0; Indels 0; Gaps 0;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTMWANTKEVCGSIKIYQEKWKHLYLVNCGSPGNFKNEELYQTK 49
 Db 1 HYTMWANTKEVCGSIKIYQEKWKHLYLVNCGSPGNFKNEELYQTK 49

RESULT 2
 AAY45217
 ID AAY45217 standard; protein; 204 AA.
 XX AC AAY45217;
 XX AC AAY45217;
 XX DT 05-JAN-2000 (first entry)
 XX DE Wild type wasp Ves v 5 protein sequence.
 XX Bet v 1; Ves v 5; pollen allergen; Fagales; Oleales; Piniales; mutant;
 KW Hymenoptera; IGE; immunoglobulin E; vaccine; allergic reaction.
 XX Vesputia lewisii.
 OS WO9947680-A1.
 XX PN 23-SEP-1999.
 XX PD 16-MAR-1999; 99WO-DK000136.
 XX PF 16-MAR-1998; 98DK-00000364.
 XX PR (ALKA-) ALK-ABELLO AS.
 XX PA Ipsen HH, Spangfort MD, Larsen JN;
 XX WPI; 1999-601103/51.
 XX DR N-PSDB; AA225685.
 XX PT New mutated allergen with lower specific affinity to IGE, useful for
 PT treatment of allergic reactions.
 XX Example 1; Fig 13; 77pp; English.
 XX The present invention describes a recombinant mutated allergen, with a
 CC surface exposed substituted amino acid on a B-cell epitope. The
 CC recombinant, non-natural, mutated allergen has at least one surface-
 CC exposed conserved amino acid of a B-cell epitope substituted by another
 CC amino acid, and essentially the same alpha-carbon backbone tertiary
 CC structure as the naturally occurring allergen. The substituted amino acid
 CC does not occur in the same position of any known homologous protein
 CC within the taxonomic order of the natural allergen. Specific IGE binding
 CC to the mutant is reduced compared to the naturally occurring allergen.
 CC The recombinant allergen is used as a vaccine to treat, prevent or
 CC alleviate allergic reactions. The present sequence represents the wild
 CC type Ves v 5, which can have the following mutations: Lys72Ala and
 CC Tyr96Ala
 XX Sequence 204 AA;
 SQ Query Match 100.0%; Score 285; DB 2; Length 204;
 Best Local Similarity 100.0%; Pred. No. 2.9e-31;
 Matches 49; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HYTMWANTKEVCGSIKIYQEKWKHLYLVNCGSPGNFKNEELYQTK 49
 Db 156 HYTMWANTKEVCGSIKIYQEKWKHLYLVNCGSPGNFKNEELYQTK 204

RESULT 3

ABG66977
 XX ID ABG66977 standard; protein; 204 AA.
 XX AC ABG66977;
 XX DT 24-SEP-2002 (first entry)
 XX DE Wasp venom antigen 5 mutant K29A.
 XX Immunoglobulin E; IGE; allergen; allergy; mite; hay fever;
 KW rhinoconjunctivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
 KW vaccine; antiallergic; B cell epitope.
 XX Vesputia vulgaris.
 OS Synthetic.
 XX PN WO200240676-A2.
 XX PD 23-MAY-2002.
 XX PF 16-NOV-2001; 2001WO-DK000764.
 XX PR 16-NOV-2000; 2000DK-00001718.
 XX PR 16-NOV-2000; 2000US-0249361P.
 XX PR 14-JUN-2001; 2001US-0298170P.
 XX PA (ALKA-) ALK-ABELLO AS.
 XX Holm J, Ipsen H, Nedergaard Larsen J, Spangfort MD;
 XX WPI; 2002-508328/54.
 XX DR New recombinant mutant allergen, useful for preventing and/or treating
 XX PT allergy, comprises multiple mutations and reduced immunoglobulin E
 XX PT binding affinity.
 XX Example 3; Page: 210pp; English.
 XX The invention relates to a recombinant allergen (I) which is a mutant of
 CC a naturally occurring allergen, where the mutant allergen has at least
 CC four primary mutations, which each reduce the specific immunoglobulin E
 CC (IGE) binding capability of the mutated allergen as compared to the IGE
 CC binding capability of the naturally occurring allergen, where each
 CC primary mutation is a substitution of one surface-exposed amino acid
 CC residue with another residue, which does not occur in the same position
 CC in the amino acid sequence of any known homologous protein within the
 CC taxonomic species from which the naturally occurring allergen originates,
 CC and each primary mutation is spaced from each other primary mutation by
 CC at least 15 Angstrom, and the primary mutations are placed in such a
 CC manner that at least one circular surface region with a area of 800
 CC Angstrom² comprises no mutation. Also included are a composition
 CC comprising two or more of the recombinant allergens, where the variant
 CC allergen is defined by having at least one primary mutation, which is
 CC absent in at least one of the other variants, and for each variant no
 CC secondary mutation is present within a radius of 15 Angstrom from each
 CC absent primary mutation; a DNA sequence encoding the recombinant allergen
 CC or its derivative, partial sequence or degenerated sequence, where the
 CC sequence which hybridises to it under stringent conditions, where the
 CC derivative, partial sequence, degenerated sequence or hybridising
 CC sequence encodes a peptide having at least one B cell epitope; an
 CC expression vector comprising the DNA and a host cell comprising the
 CC vector. The recombinant allergen is useful as a pharmaceutical, for
 CC preparing a pharmaceutical for preventing and/or treating allergy, or in
 CC a diagnostic assay for assessing relevance, safety or outcome of therapy
 CC of a subject, where an IGE containing sample of the subject is mixed with
 CC the recombinant allergen and assessed for the level of reactivity between
 CC the IGE in the sample and the recombinant allergen. The recombinant
 CC allergen or compositions are useful for generating an immune response in
 CC a subject, for vaccination or treatment of a subject or for the
 CC treatment, prevention or alleviation of allergic reactions in a subject
 CC e.g. hay fever, rhinoconjunctivitis, rhinitis, asthma or systemic
 CC anaphylaxis. The present sequence represents a recombinant allergen of
 CC the invention. Note: The present sequence was not shown in the

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:52:17 ; Search time 68.2634 Seconds
(without alignments)
315.390 Million cell updates/sec

Title: US-10-091-135-8

Perfect score: 285

Sequence: 1 HYTQMVMANTKEVCGSIKY.....LVCNYGSPGNKNEELYQTK 49

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	285	100.0	49	AAE28814	Vesputa v
2	285	100.0	204	AAV45217	Wild type
3	285	100.0	204	ABG66977	Wasp veno
4	285	100.0	204	ABG66983	Wasp veno
5	285	100.0	204	ABG67052	Wasp veno
6	285	100.0	204	ABG67104	Wasp veno
7	285	100.0	204	ABG67103	Wasp veno
8	285	100.0	204	AAE28820	Vesputa v
9	285	100.0	209	ABM00031	Allergen
10	279	97.9	204	AAW35688	Vespid an
11	279	97.9	227	AAV25644	Vesputa v
12	279	97.9	227	AAE13071	Vesputa v
13	279	97.9	227	ADC34893	Wasp alle
14	276	96.8	204	AAW35687	Vespid an
15	237	83.2	206	AAV25648	Vesputa s
16	237	83.2	206	ADC34897	Wasp alle
17	226	79.3	203	AAW35689	Vespid an
18	217	76.1	205	AAW35690	Vespid an
19	210	73.7	204	AAW35691	Vespid an
20	203	71.2	125	AAV44015	White-fac
21	196	68.8	124	AAV44014	White-fac
22	189	66.3	205	AAW35693	Vespid an
23	181	63.5	205	AAW35692	Vespid an
24	181	63.5	205	AAE28821	Polistes

25	158.5	55.6	162	5	AAE21099	Aae21099 Human spe
26	135	47.4	172	4	ABU53238	Human tes
27	133.5	46.8	202	9	ADY66414	S. mansoni
28	123	43.2	220	2	AAW35678	T. cell pe
29	123	43.2	225	8	ADP43676	Human PMM
30	123	43.2	266	4	AAW39716	Human pol
31	123	43.2	270	2	AAW63115	A human p
32	123	43.2	270	6	ABU92021	Human pro
33	123	43.2	270	8	ADP07714	Human sec
34	123	43.2	270	8	ADQ65201	Novel hum
35	123	43.2	347	4	AAW41502	Human pol
36	123	43.2	347	7	ADQ65201	Novel pro
37	123	43.2	347	7	ADQ65201	Novel pro
38	123	43.2	463	2	AAV13392	Amino aci
39	123	43.2	463	2	AAW01373	Neuron-as
40	123	43.2	463	3	AAW95343	Human PRO
41	123	43.2	463	3	ADC78597	Human PRO
42	123	43.2	463	4	AAW80260	Human PRO
43	123	43.2	463	4	AAU12351	Human PRO
44	123	43.2	463	4	AAW53088	Human ang
45	123	43.2	463	4	AAW88408	Human mem

ALIGNMENTS

RESULT 1
AAE28814
ID AAE28814 standard; peptide; 49 AA.
XX
AC AAE28814;
XX
DT 27-DEC-2002 (first entry)
XX
DE Vesputa vulgaris antigen 5 (Ves V5) allergen peptide #8.
XX
KW Allergen; hybrid protein; allergenicity; immune system related disease;
KW immunogenicity; allergy; vaccine; antigen 5.
XX
OS Vesputa vulgaris.
XX
PN WO200270665-A2.
XX
PD 12-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006765.
XX
PR 02-MAR-2001; 2001US-0272818P.
XX
PA (UYRQ) UNIV ROCKEFELLER.
PA (ALKA-) ALK-ABELLO AS.
XX
PI King TP, Spangfort MD;
XX
DR WPI; 2002-698751/75.
XX
N-PSDB; RAD46232.
XX
PT New allergen hybrid protein having reduced allergenicity but retaining immunogenicity, useful for treating allergy or immune system related diseases.
XX
PS Claim 17; Page 151; 222pp; English.
XX
CC The present invention relates to recombinant allergen hybrid proteins having reduced allergenicity but retaining immunogenicity. The hybrid proteins comprise a peptide epitope sequence of an allergen protein and a scaffold protein that is structurally homologous to the allergen protein. Sequences of the invention comprise a native conformation and the peptide epitope sequence is present in a surface accessible region of the hybrid protein corresponding to its position in the allergen protein. The hybrid proteins are useful for treating allergy or immune system related diseases. They are also used as vaccines. The present sequence is Vesputa vulgaris antigen 5 (Ves V5) allergen peptide

Wed Apr 19 09:09:58 2006

```

US-11-090-439-38
; ORGANISM: Homo sapiens
; Sequence 38, Application US/11090439
; Publication No. US20050266442A1
; GENERAL INFORMATION:
; APPLICANT: Squillace, Rachel P.
; APPLICANT: Weiner, Michael P.
; TITLE OF INVENTION: Immortalized Human Tuberos Sclerosis Null
; FILE OF INVENTION: Angiomyolipoma Cell and Method of Use Thereof
; FILE REFERENCE: 24318-502
; CURRENT APPLICATION NUMBER: US/11/090,439
; CURRENT FILING DATE: 2005-03-25
; PRIOR APPLICATION NUMBER: 60/556,344
; PRIOR FILING DATE: 2004-03-25
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-090-439-38

Query Match      27.3%; Score 69.5; DB 7; Length 258;
Best Local Similarity 40.9%; Pred. No. 0.16;
Matches 18; Conservative 8; Mismatches 5; Indels 13; Gaps 3;

QY      2 VGVNVALTGSTAAKYDDPVKLVKQWEDEVKDY-----NPK 36
DB      121 LGQNLVRTG----RYRSILQLVKPWEDEVKDYAPFPQDCNPR 160

RESULT 4
US-10-453-372-98
; Sequence 98, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METHOD
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 98
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-90

Query Match      24.5%; Score 62.5; DB 6; Length 477;
Best Local Similarity 43.8%; Pred. No. 2.7;
Matches 14; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY      2 VGVNVALTGSTAAKYDDPVKLVKQWEDEVKDY 33
DB      110 IGQNL---GAHWGRYRSPGFHVQSWYDEVKDY 138

RESULT 6
US-10-453-372-92
; Sequence 92, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 98
; LENGTH: 475
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-90
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US-10-453-372-98
; ORGANISM: Homo sapiens
; Sequence 98, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 09/823187
; PRIOR FILING DATE: 2001-03-29
; PRIOR APPLICATION NUMBER: 60/195792
; PRIOR FILING DATE: 2000-03-10
; PRIOR APPLICATION NUMBER: 09/839446
; PRIOR FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 60/199476
; PRIOR FILING DATE: 2000-03-25
; PRIOR APPLICATION NUMBER: 09/863776
; PRIOR FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: 60/208263
; PRIOR FILING DATE: 2000-05-31
; PRIOR APPLICATION NUMBER: 09/939398
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 60/227800
; PRIOR FILING DATE: 2000-08-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 90
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-90

Query Match      24.5%; Score 62.5; DB 6; Length 477;
Best Local Similarity 43.8%; Pred. No. 2.7;
Matches 14; Conservative 5; Mismatches 10; Indels 3; Gaps 1;

QY      2 VGVNVALTGSTAAKYDDPVKLVKQWEDEVKDY 33
DB      110 IGQNL---GAHWGRYRSPGFHVQSWYDEVKDY 138

RESULT 6
US-10-453-372-92
; Sequence 92, Application US/10453372
; Publication No. US2006000323A1
; GENERAL INFORMATION:
; APPLICANT: Alsobrook, et al.
; TITLE OF INVENTION: THERAPEUTIC POLYPEPTIDES, NUCLEIC ACIDS ENCODING SAME, AND METH
; FILE REFERENCE: 21402-589 A
; CURRENT APPLICATION NUMBER: US/10/453,372
; CURRENT FILING DATE: 2003-06-03
; PRIOR APPLICATION NUMBER: 09/789390
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: 60/185967
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1609
; SOFTWARE: Curaseqlist version 0.1
; SEQ ID NO 90
; LENGTH: 477
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-453-372-90
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:08:42 ; Search time 11.9084 Seconds
(without alignments)
171.264 Million cell updates/sec

Title: US-10-091-135-7
Perfect score: 255
Sequence: 1 QVGQNVALTGSTAAKYDDPV.....EVKDYNPKKFSGNDFLKTG 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_New:*
1: /SIDSS5/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
2: /SIDSS5/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
3: /SIDSS5/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
4: /SIDSS5/ptodata/2/pubpaa/FCI_NEW_PUB.pep.*
5: /SIDSS5/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
6: /SIDSS5/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
7: /SIDSS5/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
8: /SIDSS5/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Score	Query Match		Length	DB	ID	Description		
			%						
1	255	100.0	227	6	US-10-498-026-76		Sequence 76, Appl		
2	148	58.0	206	6	US-10-498-026-80		Sequence 80, Appl		
3	69.5	27.3	258	7	US-11-090-439-38		Sequence 38, Appl		
4	62.5	24.5	475	6	US-10-453-372-98		Sequence 98, Appl		
5	62.5	24.5	477	6	US-10-453-372-90		Sequence 90, Appl		
6	62.5	24.5	497	6	US-10-453-372-92		Sequence 92, Appl		
7	62.5	24.5	497	6	US-10-453-372-100		Sequence 100, Appl		
8	62.5	24.5	497	6	US-10-453-372-102		Sequence 102, Appl		
9	62.5	24.5	497	6	US-10-218-784-56		Sequence 56, Appl		
10	62.5	24.5	497	6	US-10-219-061-56		Sequence 56, Appl		
11	62.5	24.5	497	6	US-10-219-062-56		Sequence 56, Appl		
12	62.5	24.5	497	6	US-10-219-064-56		Sequence 56, Appl		
13	62.5	24.5	497	6	US-10-233-134-56		Sequence 56, Appl		
14	62.5	24.5	501	6	US-10-453-372-96		Sequence 96, Appl		
15	61.5	24.1	500	6	US-10-194-487-70		Sequence 70, Appl		
16	61.5	24.1	500	6	US-10-195-883-70		Sequence 70, Appl		
17	61.5	24.1	500	6	US-10-195-888-70		Sequence 70, Appl		
18	61.5	24.1	500	6	US-10-195-889-70		Sequence 70, Appl		
19	61.5	24.1	500	7	US-11-067-573-2		Sequence 2, Appl		
20	58	22.7	76	7	US-11-079-463-8214		Sequence 8214, Appl		
21	58	22.7	379	7	US-11-096-568A-26485		Sequence 26485, Appl		
22	58	22.7	397	7	US-11-096-568A-26484		Sequence 26484, Appl		
23	58	22.7	413	7	US-11-096-568A-26483		Sequence 26483, Appl		
24	58	22.7	498	6	US-10-453-372-94		Sequence 94, Appl		
25	57.5	22.5	572	7	US-11-188-298-19935		Sequence 19935, Appl		

ALIGNMENTS

RESULT 1

US-10-498-026-76
; Sequence 76, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 76
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-76
Query Match 100.0%; Score 255; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 1e-25;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVGQNVALTGSTAAKYDDPVKLVKMWEDVKDYNPKKFSGNDFLKTG 48
Db 131 QVGQNVALTGSTAAKYDDPVKLVKMWEDVKDYNPKKFSGNDFLKTG 178

RESULT 2

US-10-498-026-80
; Sequence 80, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 80
; LENGTH: 206
; TYPE: PRT
; ORGANISM: Vespula vulgaris
US-10-498-026-80
Query Match 58.0%; Score 148; DB 6; Length 206;
Best Local Similarity 59.6%; Pred. No. 7.6e-12;
Matches 28; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

ORGANISM: Vesputula vulgaris
US-10-091-135-16
Query Match 100.0%; Score 255; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 9.4e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVGNVALTGSTAAKYDDPVLVKVWMEDEVKDYNNPKKFSGNDPLKGTG 48
DB 108 QVGNVALTGSTAAKYDDPVLVKVWMEDEVKDYNNPKKFSGNDPLKGTG 155
RESULT 3
US-10-091-135-64
Sequence 64, Application US/10091135
Publication No. US20030039660A1
GENERAL INFORMATION:
APPLICANT: King, Te Piao
APPLICANT: Spangfort, Michael Dho
TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN
FILE REFERENCE: 2313/1H587-US1
CURRENT APPLICATION NUMBER: US/10/091,135
PRIOR FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: US 60/272,818
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn version 3.1
SEQ ID NO 64
LENGTH: 204
TYPE: PRT
ORGANISM: Vesputula vulgaris
US-10-091-135-64
Query Match 100.0%; Score 255; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 9.4e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVGNVALTGSTAAKYDDPVLVKVWMEDEVKDYNNPKKFSGNDPLKGTG 48
DB 108 QVGNVALTGSTAAKYDDPVLVKVWMEDEVKDYNNPKKFSGNDPLKGTG 155
RESULT 4
US-10-091-135-81
Sequence 81, Application US/10091135
Publication No. US20030039660A1
GENERAL INFORMATION:
APPLICANT: King, Te Piao
APPLICANT: Spangfort, Michael Dho
TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN
FILE REFERENCE: 2313/1H587-US1
CURRENT APPLICATION NUMBER: US/10/091,135
PRIOR FILING DATE: 2002-03-04
PRIOR APPLICATION NUMBER: US 60/272,818
PRIOR FILING DATE: 2001-03-02
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn version 3.1
SEQ ID NO 81
LENGTH: 204
TYPE: PRT
ORGANISM: Vesputula vulgaris
US-10-091-135-81
Query Match 100.0%; Score 255; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 9.4e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVGNVALTGSTAAKYDDPVLVKVWMEDEVKDYNNPKKFSGNDPLKGTG 48
DB 108 QVGNVALTGSTAAKYDDPVLVKVWMEDEVKDYNNPKKFSGNDPLKGTG 155

RESULT 5
US-10-719-553-39
Sequence 39, Application US/10719553
Publication No. US20040091500A1
GENERAL INFORMATION:
APPLICANT: Ipeen, Hans Henrik
APPLICANT: Spangfort, Michael Dho
APPLICANT: Larsen Jorgen Nedergaard
TITLE OF INVENTION: NOVEL RECOMBINANT ALLERGENS
FILE REFERENCE: 04305/100E144-US2
CURRENT APPLICATION NUMBER: US/10/719,553
CURRENT FILING DATE: 2003-11-20
PRIOR APPLICATION NUMBER: 09/270,910
PRIOR FILING DATE: 1999-03-16
PRIOR APPLICATION NUMBER: 60/078,371
PRIOR FILING DATE: 1998-03-18
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 39
LENGTH: 204
TYPE: PRT
ORGANISM: vesputula vulgaris
US-10-719-553-39
Query Match 100.0%; Score 255; DB 4; Length 204;
Best Local Similarity 100.0%; Pred. No. 9.4e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVGNVALTGSTAAKYDDPVLVKVWMEDEVKDYNNPKKFSGNDPLKGTG 48
DB 108 QVGNVALTGSTAAKYDDPVLVKVWMEDEVKDYNNPKKFSGNDPLKGTG 155
RESULT 6
US-09-957-806A-22
Sequence 22, Application US/09957806A
Publication No. US20050181446A1
GENERAL INFORMATION:
APPLICANT: Roggen, Erwin
APPLICANT: Ernst, Steffen
APPLICANT: Svendsen, Allan
APPLICANT: Friis, Esben
APPLICANT: Otten, Claus
TITLE OF INVENTION: PROTEIN VARIANTS HAVING MODIFIED IMMUNOGENICITY
FILE REFERENCE: 10021.204-US
CURRENT APPLICATION NUMBER: US/09/957,806A
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 248
SOFTWARE: PatentIn version 3.1
SEQ ID NO 22
LENGTH: 209
TYPE: PRT
ORGANISM: Vesputula vulgaris
US-09-957-806A-22
Query Match 100.0%; Score 255; DB 3; Length 209;
Best Local Similarity 100.0%; Pred. No. 9.7e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 QVGNVALTGSTAAKYDDPVLVKVWMEDEVKDYNNPKKFSGNDPLKGTG 48
DB 113 QVGNVALTGSTAAKYDDPVLVKVWMEDEVKDYNNPKKFSGNDPLKGTG 160
RESULT 7
US-10-001-245-214
Sequence 214, Application US/10001245
Publication No. US20030175312A1
GENERAL INFORMATION:
APPLICANT: HOLM, Jens
APPLICANT: IPSEN, Henrik
APPLICANT: LARSEN, Jorgen N.

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2006, 11:05:57 ; Search time 73.4657 Seconds
(without alignments)
272.996 Million cell updates/sec

Title: US-10-091-135-7
Perfect score: 255
Sequence: 1 QVGQNVALTGSTAAKYDDPV.....EVKDYNPKKKFSGNDFLKTG 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA_Main:
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2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	255	100.0	48	4	US-10-091-135-7
2	255	100.0	204	4	US-10-091-135-16
3	255	100.0	204	4	US-10-091-135-64
4	255	100.0	204	4	US-10-091-135-81
5	255	100.0	204	4	US-10-719-533-39
6	255	100.0	209	3	US-09-957-806A-22
7	255	100.0	210	4	US-10-001-245-214
8	255	100.0	227	3	US-09-847-208-170
9	255	100.0	227	5	US-10-809-689-82
10	250	98.0	204	3	US-09-847-208-162
11	250	98.0	204	4	US-10-091-135-65
12	244	95.7	202	4	US-10-001-245-117
13	244	95.7	203	4	US-10-001-245-118
14	227.5	89.2	201	4	US-10-001-245-119
15	226	88.6	204	3	US-09-847-208-163
16	226	88.6	204	4	US-10-091-135-67
17	224	87.8	204	3	US-09-847-208-165
18	224	87.8	204	4	US-10-091-135-63
19	213	83.5	204	3	US-09-847-208-166
20	213	83.5	204	4	US-10-091-135-66
21	208	81.6	198	4	US-10-001-245-121
22	193.5	72.0	192	4	US-10-001-245-122
23	174	68.2	194	4	US-10-001-245-120
24	148	58.0	206	3	US-09-847-208-171
25	148	58.0	206	4	US-10-091-135-68
26	148	58.0	206	5	US-10-809-689-86
27	136	53.3	203	3	US-09-847-208-86

28	136	53.3	203	4	US-10-091-135-71	Sequence 71, Appl
29	133.5	52.4	205	4	US-10-091-135-72	Sequence 72, Appl
30	133.5	52.4	215	3	US-09-847-208-91	Sequence 91, Appl
31	132	51.8	204	4	US-10-091-135-70	Sequence 70, Appl
32	132	51.8	205	3	US-09-847-208-167	Sequence 167, App
33	132	51.8	205	4	US-10-091-135-69	Sequence 69, Appl
34	132	51.8	227	3	US-09-847-208-90	Sequence 90, Appl
35	112	43.9	205	3	US-09-847-208-152	Sequence 152, App
36	112	43.9	205	4	US-10-091-135-76	Sequence 76, Appl
37	103	40.4	205	3	US-09-847-208-151	Sequence 151, App
38	103	40.4	205	4	US-10-091-135-77	Sequence 77, Appl
39	101.5	39.8	202	3	US-09-847-208-160	Sequence 160, App
40	101.5	39.8	202	4	US-10-091-135-74	Sequence 74, Appl
41	99.5	39.0	206	3	US-09-847-208-150	Sequence 150, App
42	98	38.4	205	4	US-10-091-135-78	Sequence 17, Appl
43	98	38.4	205	3	US-10-091-135-78	Sequence 78, Appl
44	98	38.4	209	3	US-09-847-208-149	Sequence 149, App
45	96.5	37.8	202	3	US-09-847-208-161	Sequence 161, App

ALIGNMENTS

RESULT 1
US-10-091-135-7
; Sequence 7, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGI
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 7
; LENGTH: 48
; TYPE: PRT
; ORGANISM: Vesputia vulgaris
US-10-091-135-7

Query Match	100.0%	Score 255;	DB 4;	Length 48;
Best Local Similarity	100.0%;	Pred. No. 1.7e-26;		
Matches 48;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	QVGQNVALTGSTAAKYDDPVKLVQWDEVDKYNPKKFSGNDFLKTG 48		
Db	1	QVGQNVALTGSTAAKYDDPVKLVQWDEVDKYNPKKFSGNDFLKTG 48		

RESULT 2
US-10-091-135-16
; Sequence 16, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGI
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091,135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272,818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 204
; TYPE: PRT

STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,287
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-156 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Vesputula vulgaris
US-09-130-287-2
Query Match 100.0%; Score 255; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.2e-28;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QVGNVALTGTAAKYDDPVKLVKWEDEVKDYNNPKKFKSGNDFLKTG 48
Db 108 QVGNVALTGTAAKYDDPVKLVKWEDEVKDYNNPKKFKSGNDFLKTG 155
RESULT 4
US-09-541-759-6
Sequence 6, Application US/09541759
Patent No. 6723322
GENERAL INFORMATION:
APPLICANT: Lustigman, Sara
APPLICANT: Pearlman, Eric
APPLICANT: Unnasch, Thomas
TITLE OF INVENTION: ANGIOGENIC ONCHOCERCA VOLVULUS PROTEINS AND USES THEREOF
FILE REFERENCE: 63475/252
CURRENT APPLICATION NUMBER: US/09/541,759
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 21
SOFTWARE: Patent in version 3.0
SEQ ID NO 6
LENGTH: 227
TYPE: PRT
ORGANISM: Vesputula vulgaris
US-09-541-759-6
Query Match 100.0%; Score 255; DB 2; Length 227;
Best Local Similarity 100.0%; Pred. No. 2.5e-28;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVGNVALTGTAAKYDDPVKLVKWEDEVKDYNNPKKFKSGNDFLKTG 48
Db 108 QVGNVALTGTAAKYDDPVKLVKWEDEVKDYNNPKKFKSGNDFLKTG 155
RESULT 2
US-08-614-935-2
Sequence 2, Application US/08614935
Patent No. 5804201
GENERAL INFORMATION:
APPLICANT: King, Te P.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-156
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 204 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE:
ORIGINAL SOURCE:
ORGANISM: Vesputula vulgaris
US-08-614-935-2
Query Match 100.0%; Score 255; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.2e-28;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 QVGNVALTGTAAKYDDPVKLVKWEDEVKDYNNPKKFKSGNDFLKTG 48
Db 108 QVGNVALTGTAAKYDDPVKLVKWEDEVKDYNNPKKFKSGNDFLKTG 155
RESULT 3
US-09-130-287-2
Sequence 2, Application US/09130287
Patent No. 6106844
GENERAL INFORMATION:
APPLICANT: King, Te P.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:57:41 ; Search time 14.4733 Seconds
(without alignments)
274.190 Million cell updates/sec

Title: US-10-091-135-7

Perfect score: 255

Sequence: 1 QVGQNVALTGSTAAKYDDPV.....EVKYNPKKXFGNDFLKTG 48

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : Issued Patents AA:**

- 1: /cgn2_6/ptodata/1/1aa/5-COMB.pep:**
- 2: /cgn2_6/ptodata/1/1aa/6-COMB.pep:**
- 3: /cgn2_6/ptodata/1/1aa/H-COMB.pep:**
- 4: /cgn2_6/ptodata/1/1aa/PCTUS-COMB.pep:**
- 5: /cgn2_6/ptodata/1/1aa/RE-COMB.pep:**
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:**

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	255	100.0	204	1	US-08-419-414-9 Sequence 9, Appli
2	255	100.0	204	1	US-08-614-935-2 Sequence 2, Appli
3	255	100.0	204	2	US-09-130-287-2 Sequence 2, Appli
4	255	100.0	227	2	US-09-541-759-6 Sequence 6, Appli
5	224	87.8	204	1	US-08-614-935-1 Sequence 1, Appli
6	224	87.8	204	2	US-09-130-287-1 Sequence 1, Appli
7	136	53.3	203	1	US-08-419-414-8 Sequence 8, Appli
8	136	53.3	203	1	US-08-614-935-3 Sequence 3, Appli
9	136	53.3	203	2	US-09-130-287-3 Sequence 3, Appli
10	133.5	52.4	125	1	US-07-857-2248-114 Sequence 114, App
11	132.5	52.0	205	1	US-08-614-935-4 Sequence 4, Appli
12	132.5	52.0	205	2	US-09-130-287-4 Sequence 4, Appli
13	132	51.8	124	1	US-07-857-2248-113 Sequence 113, App
14	132	51.8	166	2	US-08-614-935-30 Sequence 30, Appl
15	132	51.8	166	2	US-09-130-287-30 Sequence 30, Appl
16	132	51.8	204	1	US-08-614-935-5 Sequence 5, Appli
17	132	51.8	204	2	US-09-130-287-5 Sequence 5, Appli
18	103	40.4	205	1	US-08-614-935-7 Sequence 7, Appli
19	98	38.4	205	2	US-09-130-287-7 Sequence 7, Appli
20	98	38.4	205	1	US-08-419-414-10 Sequence 10, Appli
21	98	38.4	205	2	US-08-614-935-6 Sequence 6, Appli
22	98	38.4	205	2	US-09-130-287-6 Sequence 6, Appli
23	82	32.2	25	1	US-08-614-935-69 Sequence 69, Appl
24	82	32.2	25	2	US-09-130-287-69 Sequence 69, Appl
25	65	25.5	20	1	US-08-614-935-20 Sequence 20, Appl
26	65	25.5	20	2	US-09-130-287-20 Sequence 20, Appl
27	63	24.7	25	1	US-08-614-935-68 Sequence 68, Appl

Query Match 100.0%; Score 255; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.2e-28;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

28	63	24.7	25	2	US-09-130-287-68	Sequence 68, Appli
29	61.5	24.1	500	2	US-09-939-833A-363	Sequence 363, App
30	61.5	24.1	500	2	US-10-020-445A-363	Sequence 363, App
31	59	23.1	108	1	US-08-828-239-4	Sequence 4, Appli
32	59	23.1	108	2	US-09-205-679-4	Sequence 4, Appli
33	57	22.4	69	2	US-09-513-999C-5968	Sequence 5968, Ap
34	57	22.4	106	2	US-09-513-999C-5967	Sequence 5967, Ap
35	57	22.4	108	1	US-08-828-239-3	Sequence 3, Appli
36	57	22.4	108	2	US-09-205-679-3	Sequence 3, Appli
37	57	22.4	108	2	US-09-513-999C-8086	Sequence 8086, Ap
38	57	22.4	108	2	US-09-949-016-11049	Sequence 11049, A
39	56	22.0	20	1	US-08-614-935-19	Sequence 19, Appl
40	56	22.0	20	2	US-09-130-287-19	Sequence 19, Appl
41	56	22.0	369	2	US-03-668-097A-30	Sequence 30, Appl
42	56	22.0	394	2	US-09-248-736A-19047	Sequence 19047, A
43	55.5	21.8	122	2	US-09-513-999C-4966	Sequence 4966, Ap
44	55.5	21.8	200	2	US-09-702-705-789	Sequence 789, App
45	55.5	21.8	200	2	US-09-736-457-789	Sequence 789, App

ALIGNMENTS

RESULT 1
US-08-419-414-9
; Sequence 9, Application US/08419414
; Patent No. 5753787
; GENERAL INFORMATION:
; APPLICANT: Hawdon, John M.
; APPLICANT: Hotez, Peter J.
; APPLICANT: Jones, Brian F.
; TITLE OF INVENTION: Hookworm Vaccine
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA: US/08/419,414
; APPLICATION NUMBER: US/08/419,414
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO.: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Vespula vulgaris
US-08-419-414-9

CC use as long as its content is in no way modified and this statement is not removed.

CC -----

CC PIR; A44583; A44583.

CC HSP; Q05110; IQNX.

CC SMR; P35783; 1-204.

CC InterPro; IPR001283; Allrgn_V5/Tpx1.

CC InterPro; IPR002413; V5_allergen.

CC Pfam; PF00188; SCP; 1.

CC PRINTS; PR00838; VSALLERGEN.

CC PRINTS; PR00837; V5TPXLIKE.

CC ProDom; PD000542; Allrgn_V5/Tpx1; 1.

CC SMART; SM00198; SCP; 1.

CC PROSITE; PS01009; CRISP_1; 1.

CC PROSITE; PS01010; CRISP_2; 1.

CC Allergen; Direct protein sequencing.

FT DISULFID 4 17 By similarity.

FT DISULFID 8 101 By similarity.

FT DISULFID 26 94 By similarity.

FT DISULFID 170 187 By similarity.

SQ SEQUENCE 204 AA; 23274 MW; 7667232536AB2FC5 CRC64;

Query Match 98.0%; Score 250; DB 1; Length 204;

Best Local Similarity 97.9%; Pred. NO. 1.2e-22;

Matches 47; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 QVGNVALTGTAARYDDPVKLVQWDEVDKYNPKKFGSGNDPLKGTG 48

DB 108 QVGNVALTGTAARYDDPVKLVQWDEVDKYNPKKFGSGNNFLKGTG 155

RESULT 3

VA5_VESFE STANDARD; PRT; 204 AA.

AC P35783;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Venom allergen 5 (Antigen 5) (Ags) (Allergen Ves 5) (Ves g V).

OS Vespula germanica (Yellow jacket) (Wasp).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;

OC Vespidae; Vespinae; Vespula.

OX NCBI_TaxID=30212;

RN [1]

RP PROTEIN SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=94044316; PubMed=8227862;

RA Hoffman D.R.;

RT "Allergens in Hymenoptera venom. XXV: the amino acid sequences of antigen 5 molecules and the structural basis of antigenic cross-reactivity."

RL J. Allergy Clin. Immunol. 92:707-716(1993).

CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.

CC -!- ALLERGEN: Causes an allergic reaction in human.

CC -!- SIMILARITY: Belongs to the CRISP family.

CC -----

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC -----

CC PIR; B44583; B44583.

CC HSP; Q05110; IQNX.

CC SMR; P35784; 1-204.

CC InterPro; IPR001283; Allrgn_V5/Tpx1.

CC InterPro; IPR002413; V5_allergen.

CC Pfam; PF00188; SCP; 1.

CC PRINTS; PR00838; VSALLERGEN.

CC PRINTS; PR00837; V5TPXLIKE.

CC ProDom; PD000542; Allrgn_V5/Tpx1; 1.

CC SMART; SM00198; SCP; 1.

FT DISULFID 31 124 By similarity.

FT DISULFID 49 117 By similarity.

FT DISULFID 193 210 By similarity.

FT CONFLICT 109 109 V -> I (in Ref. 2).

FT CONFLICT 118 118 Q -> E (in Ref. 2).

FT CONFLICT 173 173 D -> N (in Ref. 2).

FT CONFLICT 219 219 M -> K (in Ref. 2).

FT HELIX 26 28

FT TURN 32 33

FT TURN 38 41

FT HELIX 38 41

FT STRAND 53 57

FT TURN 61 79

FT TURN 80 81

FT TURN 87 88

FT STRAND 94 94

FT STRAND 101 102

FT HELIX 104 114

FT TURN 115 116

FT STRAND 133 141

FT HELIX 149 157

FT HELIX 158 162

FT TURN 165 166

FT HELIX 169 171

FT HELIX 174 183

FT TURN 184 184

FT TURN 186 187

FT STRAND 190 200

FT TURN 201 202

FT STRAND 203 213

FT TURN 219 220

FT STRAND 226 227

SQ SEQUENCE 227 AA; 25798 MW; 99E9813740A66F55 CRC64;

Query Match 100.0%; Score 255; DB 1; Length 227;

Best Local Similarity 100.0%; Pred. No. 3.4e-23;

Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 QVGNVALTGTAARYDDPVKLVQWDEVDKYNPKKFGSGNDPLKGTG 48

DB 131 QVGNVALTGTAARYDDPVKLVQWDEVDKYNPKKFGSGNDPLKGTG 178

RESULT 2

VA5_VESFL STANDARD; PRT; 204 AA.

AC P35783;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Venom allergen 5 (Antigen 5) (Ags) (Allergen Ves f 5) (Ves f V).

OS Vespula flavopilosa (Yellow jacket) (Wasp).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;

OC Vespidae; Vespinae; Vespula.

OX NCBI_TaxID=30211;

RN [1]

RP PROTEIN SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=94044316; PubMed=8227862;

RA Hoffman D.R.;

RT "Allergens in Hymenoptera venom. XXV: the amino acid sequences of antigen 5 molecules and the structural basis of antigenic cross-reactivity."

RL J. Allergy Clin. Immunol. 92:707-716(1993).

CC -!- FUNCTION: May have an ancestral function in the promotion of ovum fertilization by sperm.

CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.

CC -!- ALLERGEN: Causes an allergic reaction in human.

CC -!- SIMILARITY: Belongs to the CRISP family.

CC -----

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its

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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:53:37 ; Search time 70.9008 Seconds
(without alignments) 477.644 Million cell updates/sec

Title: US-10-091-135-7

Perfect score: 255

Sequence: 1 QVGQNVALTGSTAAKYDDPV.....EVKDYNPKKKFSGNDFLKTG 48

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of bits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Minimum DB seq length: 200000000
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

**FOOT-PROCESSING: Minimum Match 0%
Maximum Match 100%**

Listing first 45 summaries

Database : UniProt 05.80:*

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1: uniprot_sprot:*
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2: uniprot_trembl:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query			DB	ID	Description
		Match	Length				
1	255	100.0	227	1	VA5_VESVU	Q05110 vespula vul	
2	250	98.0	204	1	VA5_VESPL	P35783 vespula fla	
3	226	88.6	204	1	VA5_VESGE	P35784 vespula ger	
4	224	87.8	204	1	VA5_VESNC	P35760 vespula mac	
5	213	83.5	204	1	VA5_VESPE	P35785 vespula pen	
6	148	58.0	206	1	VA5_VESVI	P35787 vespula vid	
7	136	53.3	203	1	VA5_DOLAR	Q05108 dolichovesp	
8	133.5	52.4	215	1	VA53_DOLMA	P10737 dolichovesp	
9	132	51.8	205	1	VA5_VESSQ	P35786 vespula squ	
10	132	51.8	227	1	VA53_DOLMA	P10736 dolichovesp	
11	112	43.9	205	1	VA5_POLFR	P35780 polistes fu	
12	110.5	43.3	207	1	VA5_POLSR	Q72156 polybia scu	
13	103	40.4	205	1	VA5_POLRX	P35759 polistes ex	
14	103	40.4	226	2	Q68KJ9_POLEX	Q68KJ9 polistes ex	
15	101.5	39.8	202	1	VA51_VESCR	P35781 vespa crabr	
16	99.5	39.0	206	1	VA5_POLDO	P81456 polistes do	
17	99.5	39.0	206	1	VA5_POLGA	P83377 polistes ga	
18	99.5	39.0	227	2	Q68KJ8_POLDO	Q68KJ8 polistes do	
19	98	38.4	209	1	VA5_POLAN	Q05109 polistes an	
20	96.5	37.8	202	1	VA52_VESCR	P35782 vespa crabr	
21	95	37.3	202	1	VA5_VESNA	P81657 vespa manda	
22	80	31.4	234	1	VA3_SOLIN	P35778 solenopsis	
23	71.5	28.0	280	2	Q7T141_BRARE	Q7T141 brachydanto	
24	71.5	28.0	896	2	Q9FV23_ARATH	Q9F123 arabidopsis n	
25	70.5	27.6	506	2	Q4S1C8_TETNG	Q4S1C8 tetraodon n	
26	69.5	27.3	258	2	Q43692_HUMAN	Q43692 homo sapien	
27	69.5	27.3	258	2	Q99MW7_MOUSE	Q99mw7 mus musculu	
28	69.5	27.3	258	2	Q98ST6_CHICK	Q98st6 gallus galli	
29	69.5	27.3	269	2	Q8BS03_MOUSE	Q8bs03 mus musculu	
30	69.5	27.3	295	2	Q4SMW6_TETNG	Q4smw6 tetraodon n	
31	69.5	27.3	360	2	Q75P80_ASHGO	Q75f80 ashbya goss	

32	66.5	26.1	473	2	Q4SNW7_TETNG
33	66	25.9	211	1	VA3_SOURI
34	65.5	25.7	500	2	Q4V9Y5_XENTR
35	64	25.1	1005	2	Q6N602_RHOPA
36	63.5	24.9	619	2	Q8UEZ8_AGRF5
37	63.5	24.9	637	2	Q7CYW3_AGRF5
38	63	24.7	107	2	Q4RY34_TETNG
39	63	24.7	112	2	Q6NYF7_BRARE
40	63	24.7	260	2	Q7Z0B5_STOCA
41	63	24.7	846	2	Q5Y818_9BACT
42	63	24.7	938	2	Q600F3_MYCHY
43	62.5	24.5	258	2	Q6SFU9_CANGA
44	62.5	24.5	316	2	Q6CSV2_YARLI
45	62.5	24.5	371	2	Q96K61_HUMAN

RESULT 1

VA5_VESVU STANDARD; PRT; 227 AA.

AC Q05110; Q9UB91;

DT 01-FEB-1994 (Rel. 28, Created)

DT 01-FEB-1994 (Rel. 28, Last sequence update)

DT 10-MAY-2005 (Rel. 47, Last annotation update)

DE Venom allergen 5 precursor (Antigen 5) (Ag5) (Allergen Ves v 5) (Ves v 5)

DE V.

OS Vespa vulgaris (Yellow jacket) (Wasp).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; Cecipidae; Vespinae; Vespula.

OX NCBI_TaxID=7454;

[1]

RP NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=93203603; PubMed=8454859;

RA Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;

RT "Sequence analysis and antigenic cross-reactivity of a venom allergen, Antigen 5, from hornets, wasps, and yellow jackets.";

RL J. Immunol. 150:2823-2830(1993).

[2]

RP NUCLEOTIDE SEQUENCE OF 24-227.

RA Suck R., Hagen S., Fiebig H.;

RT "Molecular cloning of a genomic sequence from the venom allergen Antigen 5 from Vespula vulgaris.";

RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.

CC -1- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.

CC -1- ALLELGEN: Causes an allergic reaction in human.

CC -1- SIMILARITY: Belongs to the CRISP family.

CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.

CC -----

DR EMBL; J98858; AAA30333.1; -, mRNA.

DR EMBL; AJ238849; CAB42887.1; -, Genomic DNA.

DR PDB; 1QNX; X-ray; A=24-227.

DR InterPro; IPR001283; Allrgn_V5/Tpx1.

DR InterPro; IPR002413; V5_allergen.

DR Pfam; PF00188; SCP; 1.

DR PRINTS; PR00838; VSALLERGEN.

DR PRINTS; PR00837; V5TPXLKE.

DR PRODOM; PD000542; Allrgn_V5/Tpx1; 1.

DR SMART; SM00198; SCP; 1.

DR PROSITE; PS01009; CRISP_1; 1.

DR PROSITE; PS01010; CRISP_2; 1.

KW 3D-structure; Allergen; Direct protein sequencing; Signal.

FT SIGNAL 1 23

FT CHAIN 24 227

FT DISULFID 27 40

FT By similarity.

FT Venom allergen 5.

RESULT 3
B37329
antigen 5 - eastern yellowjacket
C;Species: Vespula maculifrons (eastern yellowjacket)
C;Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C;Accession: B37329
R;Lu, G.; Villalba, M.; Coscia, M.R.; Hoffman, D.R.; King, T.P.
submitted to the Protein Sequence Database, August 1992
A;Reference number: A37329
A;Accession: B37329
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-204 <LUI>
A;Cross-references: UNIPROT:P35760; UNIPARC:UPI0000138092
C;Superfamily: yellowjacket venom allergen antigen 5

Query Match 87.8%; Score 224; DB 2; Length 204;
Best Local Similarity 89.6%; Pred. No. 3, 9e-20;
Matches 43; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 QVGQNVALTGSTAAKYDDPVKLVKRWEDVKDYNPKKKFSGNDFLKGTG 48
| | | | | : | | | | | : | | | | | : | | | | |
DB 108 QVGQNVALTGSTAAVNDPVLKLVKRWEDVKDYNPKKKFSNNFLKIG 155
| | | | | : | | | | | : | | | | | : | | | | |

RESULT 4
C44583
venom allergen Ves p 5 - western yellowjacket
C;Species: Vespula pensylvanica (western yellowjacket)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: C44583; C44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 molecules
A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: C44583
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-204 <HOF>
A;Cross-references: UNIPROT:P35785; UNIPARC:UPI0000138093
C;Superfamily: yellowjacket venom allergen antigen 5

Query Match 83.5%; Score 213; DB 2; Length 204;
Best Local Similarity 87.2%; Pred. No. 8, 8e-19;
Matches 41; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 VGQNVALTGSTAAKYDDPVKLVKRWEDVKDYNPKKKFSGNDFLKGTG 48
| | | | | : | | | | | : | | | | | : | | | | |
DB 109 VGQNVALTGSTADKYDDPVKLVKRWEDVKDYNPKKKFSNNFNKIG 155
| | | | | : | | | | | : | | | | | : | | | | |

RESULT 5
E44583
venom allergen antigen Ves vi 5 - yellowjacket (Vespula vidua)
C;Species: Vespula vidua
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: E44583; E44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 molecules
A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: E44583
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-206 <HOF>
A;Cross-references: UNIPROT:P35787; UNIPARC:UPI0000138095
C;Superfamily: yellowjacket venom allergen antigen 5

' Query Match 58.0%; Score 148; DB 2; Length 206;
Best Local Similarity 59.6%; Pred. No. 9, 2e-11;
Matches 28; Conservative 8; Mismatches 11; Indels 0; Gaps 0;

QY 2 VGQNVALTGSTAAKYDDPVKLVKRWEDVKDYNPKKKFSGNDFLKGTG 48

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:56:21 ; Search time 10.0763 Seconds
(without alignments)
459.342 Million cell updates/sec

Title: US-10-091-135-7
Perfect score: 255
Sequence: 1 QVGNVALTGSTAAKYDDPV.....EVKDYNPKKFSGNDFLKTG 48

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	250	98.0	204	2 A44583	venom allergen ant
2	226	88.6	204	2 B44583	venom allergen ant
3	224	87.8	204	2 B37329	antigen 5 - easter
4	213	83.5	204	2 C44583	venom allergen ant
5	148	58.0	206	2 E44583	venom allergen ant
6	132.5	52.0	213	2 B31085	antigen 5-3 precu
7	132	51.8	205	2 D44583	venom allergen ant
8	132	51.8	227	2 A31085	antigen 5-2 precu
9	112	43.9	205	2 F44583	venom allergen ant
10	103	40.4	205	2 A37329	antigen 5 - paper
11	101.5	39.8	202	2 G44583	venom allergen ant
12	96.5	37.8	202	2 H44583	venom allergen III
13	78	20.6	212	2 B37320	venom allergen Sol
14	66	25.9	211	2 B58853	poly-beta-hydroxyb
15	63.5	24.9	619	2 AH2773	hypothetical prote
16	63.5	24.9	637	2 F97553	hypothetical prote
17	62	24.3	273	2 AC1435	hypothetical prote
18	62	24.3	273	2 AD1077	hypothetical prote
19	61	23.9	761	2 S60992	cap-binding protei
20	60.5	23.7	206	2 JC5331	probable ubiquitin
21	60	23.5	1053	2 T06483	superfamily I DNA
22	60	23.5	1351	2 E97273	coupling factor 6
23	59	23.1	108	1 JLBO6	hypothetical prote
24	59	23.1	518	2 T24783	protein-tyrosine-p
25	58	22.7	1494	2 T14355	calcium binding pr
26	57.5	22.5	168	2 S62881	coupling factor 6
27	57	22.4	108	2 JT0563	hypothetical prote
28	57	22.4	184	2 E90335	site-specific DNA-
29	57	22.4	336	2 S04739	

30 57 22.4 411 2 T13315 hypothetical prote
31 57 22.4 457 2 T29116 hypothetical prote
32 57 22.4 1091 2 S33850 fibronectin-binding
33 56.5 22.2 925 2 G88175 protein T24H7.2 li
34 56.5 22.2 1260 2 A87046 hypothetical prote
35 56 22.0 182 2 JQ1753 hypothetical prote
36 56 22.0 386 2 T27079 hypothetical prote
37 55.5 21.8 155 2 C86637 galactose-1-phosph
38 55.5 21.8 318 2 D72283 iron(III) ABC tran
39 55.5 21.8 352 2 C82302 major capsid prote
40 55.5 21.8 531 1 P1WLHS invariant surface
41 55 21.6 436 2 A38145 deoxyribodipyrimid
42 55 21.6 484 2 S00757 two-component sens
43 55 21.6 506 2 F69867 hypothetical prote
44 55 21.6 639 2 T16648 translation initia
45 54.5 21.4 216 2 T01687

ALIGNMENTS

RESULT 1

A44583
venom allergen antigen Ves f 5 - yellowjacket (Vespula flavopilosa)
C:Species: Vespula flavopilosa
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A44583; B44522
R:Hoffman, D.R.
J: Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mol
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: A44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
A:Cross-references: UNIPROT:P35783; UNIPARC:UPI000013808F
C:Superfamily: Yellowjacket venom allergen antigen 5

Query Match 98.0%; Score 250; DB 2; Length 204;
Best Local Similarity 97.9%; Pred. No. 2.4e-23;
Matches 47; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVGNVALTGSTAAKYDDPVKLVKMWEDVKDYNPKKFSGNDFLKTG 48
Db 108 QVGNVALTGSTAAKYDDPVKLVKMWEDVKDYNPKKFSGNDFLKTG 155

RESULT 2

B44583
venom allergen antigen Ves g 5 - German yellowjacket
C:Species: Vespula germanica (German yellowjacket)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: B44583; A44522
R:Hoffman, D.R.
J: Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mol
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: B44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>
A:Cross-references: UNIPROT:P35784; UNIPARC:UPI0000138090
C:Superfamily: yellowjacket venom allergen antigen 5

Query Match 88.6%; Score 226; DB 2; Length 204;
Best Local Similarity 91.5%; Pred. No. 2.2e-20;
Matches 43; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 VGQNVALTGTAAYDDPVKLVKMWEDVKDYNPKKFSGNDFLKTG 48
Db 109 VGQNVALTGTAAYDDPVKLVKMWEDVKDYNPKKFSGNDFLKTG 155

```

XX SQ      Sequence 48 AA;
Query Match      100.0%; Score 255; DB 5; Length 48;
Best Local Similarity 100.0%; Pred. No. 3.7e-27;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVGQNVALTGSTAAKYDDPDKLVKQWEDEVKYNPKKFSGNDPLKGTG 48
    |||||
Db 1 QVGQNVALTGSTAAKYDDPDKLVKQWEDEVKYNPKKFSGNDPLKGTG 48

RESULT 2
AAW35688
ID AAW35688 standard; peptide; 204 AA.
XX
AC AAW35688;
XX
DT 13-MAY-1998 (first entry)
XX
DE Vespid antigen 5s from Vesputia vulgaris (yellowjacket).
XX
KW Immunomodulatory peptide; vespid antigen 5; immunogenic; allergy;
KW vespid venom; white face hornet wasp; immunodominant peptide; T cell.
XX
OS Vesputia vulgaris.
XX
PN WO9733910-A1.
XX
PD 18-SEP-1997.
XX
PF 11-MAR-1997; 97WO-US003753.
XX
PR 11-MAR-1996; 96US-00614935.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
XX
PI King TP;
XX
DR WPI; 1997-470817/43.
XX
PT Vespid venom antigen 5 peptide fragments - useful to treat or diagnose
PT vespid venom sensitivity.
XX
PS Example 1; Fig 1; 73pp; English.
XX
CC This sequence represents vespid antigen 5s from yellowjacket. The
CC invention relates to peptides derived from vespid venom antigen 5 (VV5)
CC that are antigenic for T cell proliferation in mice immunised with VV5.
CC The peptides can be used to treat or diagnose vespid venom sensitivity
CC e.g. to Dolichovesputia maculata (white face hornet), Vesputia vulgaris
CC (yellowjacket), V. maculifrons (yellowjacket), D. arenaria (yellow
CC hornet), Polistes annularis (wasp), P. exclamans (wasp), V. crabro
CC (European hornet), V. flavopilosa (yellowjacket), V. germanica
CC (yellowjacket), V. pennsylvanica (yellowjacket), V. squamosa
CC (yellowjacket), V. vidua (yellowjacket) and P. fuscatus (paperwasp)
XX
SQ      Sequence 204 AA;
Query Match      100.0%; Score 255; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.3e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVGQNVALTGSTAAKYDDPDKLVKQWEDEVKYNPKKFSGNDPLKGTG 48
    |||||
Db 108 QVGQNVALTGSTAAKYDDPDKLVKQWEDEVKYNPKKFSGNDPLKGTG 155

RESULT 3
AAW45217
ID AAW45217 standard; protein; 204 AA.
XX
AC AAW45217;

```

```

XX DT      05-JAN-2000 (first entry)
XX
DE Wild type wasp Ves v 5 protein sequence.
XX
KW Bet v 1; Ves v 5; pollen allergen; Fagales; Oleales; Pinales; mutant;
KW Hymenoptera; IgE; immunoglobulin E; vaccine; allergic reaction.
XX
OS Vesputia lewisii.
XX
PN WO9947680-A1.
XX
PD 23-SEP-1999.
XX
PF 16-MAR-1999; 99WO-DK000136.
XX
PR 16-MAR-1998; 98DK-00000364.
XX
PA (ALKA-) ALK-ABELLO AS.
XX
PI Ipsen HH, Spangfort MD, Larsen JN;
XX
DR WPI; 1999-601103/51.
DR N-PSDB; AA225685.
XX
PT New mutated allergen with lower specific affinity to IgE, useful for
PT treatment of allergic reactions.
XX
PS Example 1; Fig 13; 77pp; English.
XX
CC The present invention describes a recombinant mutated allergen, with a
CC surface exposed substituted amino acid on a B-cell epitope. The
CC recombinant, non-natural, mutated allergen has at least one surface-
CC exposed conserved amino acid of a B-cell epitope substituted by another
CC amino acid, and essentially the same alpha-carbon backbone tertiary
CC structure as the naturally occurring allergen. The substituted amino acid
CC does not occur in the same position of any known homologous protein
CC within the taxonomic order of the natural allergen. Specific IgE binding
CC to the mutant is reduced compared to the naturally occurring allergen.
CC The recombinant allergen is used as a vaccine to treat, prevent or
CC alleviate allergic reactions. The present sequence represents the wild
CC type Ves v 5, which can have the following mutations: Lys72Ala and
CC Tyr96Ala
XX
SQ      Sequence 204 AA;
Query Match      100.0%; Score 255; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 2.3e-26;
Matches 48; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 QVGQNVALTGSTAAKYDDPDKLVKQWEDEVKYNPKKFSGNDPLKGTG 48
    |||||
Db 108 QVGQNVALTGSTAAKYDDPDKLVKQWEDEVKYNPKKFSGNDPLKGTG 155

RESULT 4
ABG66977
ID ABG66977 standard; protein; 204 AA.
XX
AC ABG66977;
XX
DT 24-SEP-2002 (first entry)
XX
DE Wasp venom antigen 5 mutant K29A.
XX
KW Immunoglobulin E; IgE; allergen; allergy; mite; hay fever;
KW rhinoconjunctivitis; rhinitis; asthma; systemic anaphylaxis; mutant;
KW vaccine; antiallergic; B cell epitope.
XX
OS Vesputia vulgaris.
XX
PS Synthetic.
XX
PN WO200240676-A2.

```


GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:52:17 ; Search time 66.8702 Seconds
(without alignments)
315.390 Million cell updates/sec

Title: US-10-091-135-7
Perfect score: 255
Sequence: 1 QVCQNVALTGSTAAKYDDPV.....EVKDYNPKKKFSGNDFLKTG 48

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	255	100.0	48	AAE28813	Aae28813 Vesputa v
2	255	100.0	204	AAW35688	Aaw35688 Vespid an
3	255	100.0	204	AAy45217	Aay45217 Wild type
4	255	100.0	204	ABg66977	Abg66977 Wasp veno
5	255	100.0	204	ABg67052	Abg67052 Wasp veno
6	255	100.0	204	ABg67104	Abg67104 Wasp veno
7	255	100.0	204	ABg67103	Abg67103 Wasp veno
8	255	100.0	204	AAE28820	Aae28820 Vesputa v
9	255	100.0	209	ABM00031	Abm00031 Allergen
10	255	100.0	227	AAy25644	Aay25644 Vesputa s
11	255	100.0	227	AAE13071	Aae13071 Vesputa v
12	255	100.0	227	ADC34893	Adc34893 Wasp alle
13	249	97.6	204	ABg66983	Abg66983 Wasp veno
14	224	87.8	204	AAW35687	Aaw35687 Vespid an
15	148	58.0	206	AAy25648	Aay25648 Vesputa s
16	148	58.0	206	ADC34897	Adc34897 Wasp alle
17	136	53.3	203	AAW35689	Aaw35689 Vespid an
18	133.5	52.4	125	AAy44015	Aay44015 White-fac
19	132.5	52.0	205	AAW35690	Aaw35690 Vespid an
20	132	51.8	124	AAy44014	Aay44014 White-fac
21	132	51.8	204	AAW35691	Aaw35691 Vespid an
22	103	40.4	205	AAW35693	Aaw35693 Vespid an
23	98	38.4	205	AAW35692	Aaw35692 Vespid an
24	98	38.4	205	AAE28821	Aae28821 Pollistes

25	92	36.1	162	5	AAE21099	Aae21099 Human epe
26	82	32.2	25	2	AAW35671	Aaw35671 T cell pe
27	78	30.6	172	4	ABU53238	Abu53238 Human tes
28	69.5	27.3	188	2	AAW79915	Aaw79915 Human try
29	69.5	27.3	198	2	AAW79914	Aaw79914 Trypsin i
30	69.5	27.3	258	3	AAW79301	Aaw79301 Protein e
31	69.5	27.3	258	5	ABG61801	Abg61801 Prostate
32	69.5	27.3	258	5	ABG61802	Abg61802 Prostate
33	69.5	27.3	258	8	ABJ05597	Abj05597 Breast ca
34	69.5	27.3	258	8	ADRI4401	Adri4401 Human NF-
35	65.5	25.7	482	4	ABB62392	Abb62392 Drosophil
36	65.5	25.7	482	9	ADY79831	Ady79831 Amino aci
37	65	25.5	20	2	AAW35627	Aaw35627 Immunomod
38	64.5	25.3	205	8	ADX72834	Adx72834 Plant ful
39	63.5	24.9	96	8	ADN99462	Adn99462 Novel hum
40	63.5	24.9	142	4	AAU19527	Aau19527 Human dia
41	63	24.7	25	2	AAW35670	Aaw35670 T cell pe
42	62.5	24.5	241	4	AAW24028	Aaw24028 Rat EST e
43	62.5	24.5	252	5	ABB80591	Abb80591 Human ebg
44	62.5	24.5	371	4	AAW93979	Aaw93979 Human pro
45	62.5	24.5	438	5	ABB80593	Abb80593 Human ebg

ALIGNMENTS

RESULT 1
AAE28813
ID AAE28813 standard; peptide; 48 AA.
XX
AC AAE28813;
XX
DT 27-DEC-2002 (first entry)
XX
DE vesputa vulgaris antigen 5 (Ves V5) allergen peptide #7.
XX
KW Allergen; hybrid protein; allergenicity; immune system related disease;
KW immunogenicity; allergy; vaccine; antigen 5.
XX
OS Vesputa vulgaris.
XX
FN WO200270665-A2.
PD 12-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006765.
XX
PR 02-MAR-2001; 2001US-0272818P.
XX
PA (UYRQ) UNIV ROCKEFELLER.
FA (ALKA-) ALK-ABELLO AS.
XX
PI King TP, Spangfort MD;
XX
DR WPI; 2002-698751/75.
XX
N-PSDB; AAD46231.
PT New allergen hybrid protein having reduced allergenicity but retaining immunogenicity, useful for treating allergy or immune system related diseases.
XX
PS Claim 17; Page 151; 222pp; English.
CC The present invention relates to recombinant allergen hybrid proteins having reduced allergenicity but retaining immunogenicity. The hybrid proteins comprise a peptide epitope sequence of an allergen protein and a scaffold protein that is structurally homologous to the allergen protein. Sequences of the invention comprise a native conformation and the peptide epitope sequence is present in a surface accessible region of the hybrid protein corresponding to its position in the allergen protein. The hybrid proteins are useful for treating allergy or immune system related diseases. They are also used as vaccines. The present sequence is Vesputa vulgaris antigen 5 (Ves V5) allergen peptide

Publication No. US20060024692A1
GENERAL INFORMATION:
APPLICANT: Nakamura, Yusuke
APPLICANT: Daigo, Yataro
APPLICANT: Nakatsuru, Shuichi
TITLE OF INVENTION: METHOD FOR DIAGNOSING NON-SMALL CELL LUNG CANCERS
FILE REFERENCE: 082368-003500US
CURRENT FILING DATE: 2005-03-24
PRIOR APPLICATION NUMBER: PCT/JP04/04075
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: PCT/JP03/12072
PRIOR FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: US 60/555,757
PRIOR FILING DATE: 2004-03-24
PRIOR APPLICATION NUMBER: US 60/466,100
PRIOR FILING DATE: 2003-04-28
PRIOR APPLICATION NUMBER: US 60/451,374
PRIOR FILING DATE: 2003-02-28
PRIOR APPLICATION NUMBER: US 60/414,673
PRIOR FILING DATE: 2002-09-30
NUMBER OF SEQ ID NOS: 706
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 706
LENGTH: 2911
TYPE: PRT
ORGANISM: Homo sapiens
US-11-090-617-706

Query Match 26.4%; Score 58; DB 7; Length 2911;
Best Local Similarity 32.3%; Pred. No. 20;
Matches 10; Conservative 5; Mismatches 12; Indels 4; Gaps 1;

QY 4 CKIKLKGCV-----HTACKYGSCLKPNCNKV 30
DB 149 CSVRVNGGTGTCADDDHCQCKGKYGTYGQPV 179

RESULT 6
US-11-108-528-56
Sequence 56, Application US/11108528
Publication No. US20050261189A1
GENERAL INFORMATION:
APPLICANT: Larsen, Glenn
APPLICANT: Marvin, Martha
APPLICANT: Li, Dean Y.
APPLICANT: Wang, Elizabeth
APPLICANT: Chen, C. M. Amy
APPLICANT: Shamah, Steven M.
TITLE OF INVENTION: METHODS OF PROMOTING CARDIAC CELL
PROLIFERATION
FILE REFERENCE: HYDR-P01-041
CURRENT APPLICATION NUMBER: US/11/108,528
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US 60/563,137
PRIOR FILING DATE: 2004-04-16
PRIOR APPLICATION NUMBER: US 60/598,368
PRIOR FILING DATE: 2004-08-02
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 56
LENGTH: 365
TYPE: PRT
ORGANISM: Homo sapiens
US-11-108-528-56

Query Match 25.5%; Score 56; DB 7; Length 365;
Best Local Similarity 38.5%; Pred. No. 4.7;
Matches 10; Conservative 4; Mismatches 12; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGSCLKPNC 26
DB 199 NNLGVKVIKAGVETTCCKCHGVSGSC 224

Publication No. US20060019284A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES FOR PREDICTING ACTIVITY OF
TITLE OF INVENTION: COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE
TITLE OF INVENTION: KINASES AND/OR PROTEIN TYROSINE KINASE PATHWAYS IN LUNG CANCER
TITLE OF INVENTION: CELLS
FILE REFERENCE: 10001 NP
CURRENT APPLICATION NUMBER: US/11/169,041
CURRENT FILING DATE: 2005-06-28
PRIOR APPLICATION NUMBER: 60/584,405
PRIOR FILING DATE: 2004-06-30
NUMBER OF SEQ ID NOS: 527
SOFTWARE: PatentIn version 3.2
SEQ ID NO 131
LENGTH: 2871
TYPE: PRT
ORGANISM: Homo sapiens
US-11-169-041-131

Query Match 29.8%; Score 65.5; DB 6; Length 3002;
Best Local Similarity 25.0%; Pred. No. 1.9;
Matches 14; Conservative 8; Mismatches 13; Indels 21; Gaps 2;

QY 3 YCKIKLKGCV-----HTACKYGSCLKPNC-----NKVVVSYGLT 37
DB 118 HCNIRCMNGGSCDDHCLCKQKYGTHCGQVPCSSGCLNGRCVAPNRCACCTYGT 173

RESULT 4
US-10-821-234-916
Sequence 916, Application US/10821234
Publication No. US20050255114A1
GENERAL INFORMATION:
APPLICANT: Labat, Ivan
APPLICANT: Stache-Crain, Birgit
APPLICANT: Andarmani, Susan
APPLICANT: Tang, Y. Tom
TITLE OF INVENTION: Methods for Diagnosis and Treatment of Preeclampsia
FILE REFERENCE: 821A
CURRENT APPLICATION NUMBER: US/10/821,234
CURRENT FILING DATE: 2004-04-07
PRIOR APPLICATION NUMBER: US 60/462,047
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 1704
SOFTWARE: pt_seq_genes Version 1.0
SEQ ID NO 916
LENGTH: 3002
TYPE: PRT
ORGANISM: Homo sapiens
US-10-821-234-916

Query Match 29.8%; Score 65.5; DB 6; Length 3002;
Best Local Similarity 25.0%; Pred. No. 2;
Matches 14; Conservative 8; Mismatches 13; Indels 21; Gaps 2;

QY 3 YCKIKLKGCV-----HTACKYGSCLKPNC-----NKVVVSYGLT 37
DB 249 HCNIRCMNGGSCDDHCLCKQKYGTHCGQVPCSSGCLNGRCVAPNRCACCTYGT 304

RESULT*5
US-11-090-617-706
Sequence 706, Application US/11090617

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:08:42 ; Search time 9.67557 Seconds
(without alignments)
171.264 Million cell updates/sec

Title: US-10-091-135-5
Perfect score: 220
Sequence: 1 NNYCKIKLGGVHTACKYGLKPNCGNKVVVSYGLTKQ 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 217505 seqs, 42489236 residues

Total number of hits satisfying chosen parameters: 217505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

- Database : Published Applications AA New:*
- 1: /SIDSS/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
 - 2: /SIDSS/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
 - 3: /SIDSS/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
 - 4: /SIDSS/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
 - 5: /SIDSS/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
 - 6: /SIDSS/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
 - 7: /SIDSS/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
 - 8: /SIDSS/ptodata/2/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	220	100.0	227	6	US-10-498-026-76
2	168.5	76.6	206	6	US-10-498-026-80
3	65.5	29.8	2871	7	US-11-169-041-131
4	65.5	29.8	3002	6	US-10-821-234-916
5	58	26.4	2911	7	US-11-090-617-706
6	56	25.5	365	7	US-11-108-528-56
7	56	25.5	365	7	US-11-108-528-58
8	55	25.0	271	6	US-10-533-811-1
9	54	24.5	1294	7	US-11-079-463-7534
10	52	23.6	1978	7	US-11-212-443-60
11	51	23.2	298	7	US-11-124-367A-416
12	51	23.2	298	7	US-11-124-367A-417
13	51	23.2	298	7	US-11-124-367A-419
14	51	23.2	313	7	US-11-124-367A-418
15	51	23.2	357	7	US-11-108-528-60
16	51	23.2	359	7	US-11-108-528-62
17	51	23.2	416	7	US-11-124-367A-415
18	50	22.7	1400	6	US-10-821-234-1045
19	49.5	22.5	737	7	US-11-152-366-28
20	49	22.3	271	6	US-10-793-626-2822
21	49	22.3	271	6	US-10-793-626-3308
22	48.5	22.0	245	7	US-11-188-298-8231
23	48.5	22.0	245	7	US-11-188-298-13741
24	48.5	22.0	394	6	US-10-506-454-1398
25	48	21.8	76	6	US-10-467-657-1188

US-10-498-026-76 292 7 US-11-188-298-5690 Sequence 5690, Ap
US-10-498-026-76 602 7 US-11-096-568A-30507 Sequence 30507, A
US-10-498-026-76 701 7 US-11-096-568A-30506 Sequence 30506, A
US-10-498-026-76 879 7 US-11-096-568A-30505 Sequence 30505, A
US-10-498-026-76 124 5 US-09-995-493-84 Sequence 84, Appl
US-10-498-026-76 683 6 US-10-330-773-346 Sequence 346, App
US-10-498-026-76 702 6 US-10-330-773-341 Sequence 341, App
US-10-498-026-76 892 7 US-11-079-463-9073 Sequence 9073, Ap
US-10-498-026-76 3568 6 US-10-453-372-194 Sequence 194, App
US-10-498-026-76 3570 6 US-10-453-372-178 Sequence 178, App
US-10-498-026-76 3570 6 US-10-453-372-196 Sequence 196, App
US-10-498-026-76 3570 6 US-10-453-372-200 Sequence 200, App
US-10-498-026-76 3570 6 US-10-453-372-202 Sequence 202, App
US-10-498-026-76 3570 6 US-10-453-372-204 Sequence 204, App
US-10-498-026-76 3570 6 US-10-453-372-206 Sequence 206, App
US-10-498-026-76 50 7 US-11-172-571-5 Sequence 5, Appl
US-10-498-026-76 80 7 US-11-172-571-4 Sequence 4, Appl
US-10-498-026-76 111 7 US-11-188-298-11616 Sequence 11616, A
US-10-498-026-76 172 7 US-11-096-568A-20968 Sequence 20968, A

ALIGNMENTS

RESULT 1
US-10-498-026-76
; Sequence 76, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 76
; LENGTH: 227
; TYPE: PRT
; ORGANISM: *Vespula vulgaris*
US-10-498-026-76

Query Match 100.0%; Score 220; DB 6; Length 227;
Best Local Similarity 100.0%; Pred. No. 1.1e-22;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLGGVHTACKYGLKPNCGNKVVVSYGLTKQ 39
DB 24 NNYCKIKLGGVHTACKYGLKPNCGNKVVVSYGLTKQ 62

RESULT 2
US-10-498-026-80
; Sequence 80, Application US/10498026
; Publication No. US20060024334A1
; GENERAL INFORMATION:
; APPLICANT: CIRCASSIA LIMITED
; TITLE OF INVENTION: IMMUNOTHERAPEUTIC METHODS AND SYSTEMS
; FILE REFERENCE: N.87430 WO GCW
; CURRENT APPLICATION NUMBER: US/10/498,026
; CURRENT FILING DATE: 2004-06-04
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 80
; LENGTH: 206
; TYPE: PRT
; ORGANISM: *Vespula vulgaris*
US-10-498-026-80

Query Match 76.6%; Score 168.5; DB 6; Length 206;
Best Local Similarity 81.6%; Pred. No. 1.1e-15;
Matches 31; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

; ORGANISM: Vespula vulgaris

US-10-091-135-6

Query Match 100.0%; Score 220; DB 4; Length 46;
Best Local Similarity 100.0%; Pred. No. 3.4e-21;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCGKVKVVSGLTKQ 39
Db 1 NNYCKIKLKGCVHTACKYGLKPCGKVKVVSGLTKQ 39

RESULT 3

US-10-091-135-93

; Sequence 93, Application US/10091135

; Publication No. US20030039660A1

; GENERAL INFORMATION:

; APPLICANT: King, Te Piao

; APPLICANT: Spangfort, Michael Dho

; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED

; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN

; FILE REFERENCE: 2313/1H587-US1

; CURRENT APPLICATION NUMBER: US/10/091,135

; PRIOR FILING DATE: 2002-03-04

; PRIOR APPLICATION NUMBER: US 60/272,818

; PRIOR FILING DATE: 2001-03-02

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 93

; LENGTH: 50

; TYPE: PRT

; ORGANISM: Vespula vulgaris

US-10-091-135-93

Query Match 100.0%; Score 220; DB 4; Length 50;

Best Local Similarity 100.0%; Pred. No. 3.7e-21;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCGKVKVVSGLTKQ 39
Db 1 NNYCKIKLKGCVHTACKYGLKPCGKVKVVSGLTKQ 39

RESULT 4

US-10-091-135-94

; Sequence 94, Application US/10091135

; Publication No. US20030039660A1

; GENERAL INFORMATION:

; APPLICANT: King, Te Piao

; APPLICANT: Spangfort, Michael Dho

; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED

; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN

; FILE REFERENCE: 2313/1H587-US1

; CURRENT APPLICATION NUMBER: US/10/091,135

; PRIOR FILING DATE: 2002-03-04

; PRIOR APPLICATION NUMBER: US 60/272,818

; PRIOR FILING DATE: 2001-03-02

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 94

; LENGTH: 57

; TYPE: PRT

; ORGANISM: Vespula vulgaris

US-10-091-135-94

Query Match 100.0%; Score 220; DB 4; Length 57;

Best Local Similarity 100.0%; Pred. No. 4.3e-21;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCGKVKVVSGLTKQ 39
Db 1 NNYCKIKLKGCVHTACKYGLKPCGKVKVVSGLTKQ 39

RESULT 5

US-10-091-135-95

; Sequence 95, Application US/10091135

; Publication No. US20030039660A1

; GENERAL INFORMATION:

; APPLICANT: King, Te Piao

; APPLICANT: Spangfort, Michael Dho

; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED

; TITLE OF INVENTION: ALLERGENICITY THAT RETAIN IMMUNOGENICITY OF THE NATURAL ALLERGEN

; FILE REFERENCE: 2313/1H587-US1

; CURRENT APPLICATION NUMBER: US/10/091,135

; CURRENT FILING DATE: 2002-03-04

; PRIOR APPLICATION NUMBER: US 60/272,818

; PRIOR FILING DATE: 2001-03-02

; NUMBER OF SEQ ID NOS: 98

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 95

; LENGTH: 76

; TYPE: PRT

; ORGANISM: Vespula vulgaris

US-10-091-135-95

Query Match 100.0%; Score 220; DB 4; Length 76;

Best Local Similarity 100.0%; Pred. No. 5.8e-21;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCGKVKVVSGLTKQ 39
Db 1 NNYCKIKLKGCVHTACKYGLKPCGKVKVVSGLTKQ 39

RESULT 6

US-10-001-245-119

; Sequence 119, Application US/10001245

; Publication No. US20030175312A1

; GENERAL INFORMATION:

; APPLICANT: HOLM, Jens

; APPLICANT: IPSEN, Henrik

; APPLICANT: LARSEN, Jorgen N.

; APPLICANT: SPANGFORT, Michael D.

; TITLE OF INVENTION: No. US20030175312A1el mutant allergene

; FILE REFERENCE: 4305/1H942-US2

; CURRENT APPLICATION NUMBER: US/10/001,245

; CURRENT FILING DATE: 2001-11-15

; PRIOR APPLICATION NUMBER: US 60/298,170

; PRIOR FILING DATE: 2001-06-14

; PRIOR APPLICATION NUMBER: US 60/249,361

; PRIOR FILING DATE: 2000-11-16

; NUMBER OF SEQ ID NOS: 217

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 119

; LENGTH: 201

; TYPE: PRT

; ORGANISM: Vespula

; FEATURE:

; NAME/KEY: MISC FEATURE

; LOCATION: (1)-(201)

; OTHER INFORMATION: where X is any amino acid

US-10-001-245-119

Query Match 100.0%; Score 220; DB 4; Length 201;

Best Local Similarity 100.0%; Pred. No. 1.6e-20;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCGKVKVVSGLTKQ 39
Db 1 NNYCKIKLKGCVHTACKYGLKPCGKVKVVSGLTKQ 39

RESULT 7

US-10-001-245-117

; Sequence 117, Application US/10001245

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 11:05:57 ; Search time 59.6908 Seconds
(without alignments)
272.996 Million cell updates/sec

Title: US-10-091-135-5
Perfect score: 220
Sequence: 1 NNYCKIKLGGVHTACKYGSILKPNCGNKVVSGLTKQ 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues
Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA Main:
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	220	100.0	39	4 US-10-091-135-5	Sequence 5, Appli
2	220	100.0	46	4 US-10-091-135-6	Sequence 6, Appli
3	220	100.0	50	4 US-10-091-135-93	Sequence 93, Appl
4	220	100.0	57	4 US-10-091-135-94	Sequence 94, Appl
5	220	100.0	76	4 US-10-091-135-95	Sequence 95, Appl
6	220	100.0	201	4 US-10-091-245-119	Sequence 119, App
7	220	100.0	202	4 US-10-091-245-117	Sequence 117, App
8	220	100.0	203	4 US-10-091-245-118	Sequence 118, App
9	220	100.0	204	3 US-09-847-208-162	Sequence 162, App
10	220	100.0	204	4 US-10-091-135-16	Sequence 16, Appl
11	220	100.0	204	4 US-10-091-135-64	Sequence 64, Appl
12	220	100.0	204	4 US-10-091-135-65	Sequence 65, Appl
13	220	100.0	204	4 US-10-091-135-81	Sequence 81, Appl
14	220	100.0	204	4 US-10-719-553-39	Sequence 39, Appl
15	220	100.0	209	3 US-09-357-806A-22	Sequence 22, Appl
16	220	100.0	210	4 US-10-091-245-214	Sequence 214, App
17	220	100.0	227	5 US-09-847-208-170	Sequence 170, App
18	220	100.0	227	5 US-10-809-689-82	Sequence 82, Appl
19	216	98.2	204	3 US-09-847-208-166	Sequence 166, App
20	216	98.2	204	4 US-10-091-135-66	Sequence 66, Appl
21	214	97.3	204	3 US-09-847-208-165	Sequence 165, App
22	214	97.3	204	4 US-10-091-135-63	Sequence 63, Appl
23	212	96.4	198	4 US-10-091-245-121	Sequence 121, App
24	205.5	93.4	194	4 US-10-091-245-120	Sequence 120, App
25	197	89.5	204	3 US-09-847-208-163	Sequence 163, App
26	197	89.5	204	4 US-10-091-135-67	Sequence 67, Appl
27	184	83.6	32	4 US-10-091-135-4	Sequence 4, Appli

28	169.5	77.0	205	3	US-09-847-208-167	Sequence 167, App
29	169.5	77.0	205	4	US-10-091-135-69	Sequence 69, Appl
30	168.5	76.6	206	3	US-09-847-208-171	Sequence 171, App
31	168.5	76.6	206	4	US-10-091-135-68	Sequence 68, Appl
32	168.5	76.6	206	5	US-10-809-689-86	Sequence 86, Appl
33	168	76.4	166	4	US-10-091-245-124	Sequence 124, App
34	168	76.4	192	4	US-10-091-245-122	Sequence 122, App
35	160	72.7	170	4	US-10-091-245-123	Sequence 123, App
36	146	66.4	202	3	US-09-847-208-160	Sequence 160, App
37	146	66.4	202	3	US-09-847-208-161	Sequence 161, App
38	146	66.4	202	4	US-10-091-135-74	Sequence 74, Appl
39	146	66.4	202	4	US-10-091-135-75	Sequence 75, Appl
40	145	65.9	204	4	US-10-091-135-70	Sequence 70, Appl
41	145	65.9	227	3	US-09-847-208-90	Sequence 90, Appl
42	140	63.6	24	4	US-10-091-135-3	Sequence 3, Appli
43	137	62.3	202	3	US-09-847-208-172	Sequence 172, App
44	137	62.3	202	4	US-10-091-135-73	Sequence 73, Appl
45	133.5	60.7	203	3	US-09-847-208-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1
US-10-091-135-5
; Sequence 5, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091.135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272.818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; TYPE: PRT
; ORGANISM: Vesputia vulgaris
US-10-091-135-5

Query Match 100.0%; Score 220; DB 4; Length 39;
Best Local Similarity 100.0%; Pred. No. 2.9e-21;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLGGVHTACKYGSILKPNCGNKVVSGLTKQ 39
|||||
Db 1 NNYCKIKLGGVHTACKYGSILKPNCGNKVVSGLTKQ 39
|||||

RESULT 2
US-10-091-135-6
; Sequence 6, Application US/10091135
; Publication No. US20030039660A1
; GENERAL INFORMATION:
; APPLICANT: King, Te Piao
; APPLICANT: Spangfort, Michael Dho
; TITLE OF INVENTION: RECOMBINANT HYBRID ALLERGEN CONSTRUCTS WITH REDUCED
; FILE REFERENCE: 2313/1H587-US1
; CURRENT APPLICATION NUMBER: US/10/091.135
; CURRENT FILING DATE: 2002-03-04
; PRIOR APPLICATION NUMBER: US 60/272.818
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 98
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; TYPE: PRT

Qy 1 NNYCKIKLKGCVHTACKYGLKPCNGKVKVVSGLTKQ 39
 Db 1 NNYCKIKLKGCVHTACKYGLKPCNGKVKVVSGLTKQ 39

RESULT 2
 US-08-614-935-2
 ; Sequence 2, Application US/08614935
 ; Patent No. 5804201
 ; GENERAL INFORMATION:
 ; APPLICANT: King, Te P.
 ; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
 ; NUMBER OF SEQUENCES: 81
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David A. Jackson, Esq.
 ; STREET: 411 Hackensack Ave, Continental Plaza, 4th
 ; CITY: Hackensack
 ; STATE: New Jersey
 ; COUNTRY: USA
 ; ZIP: 07601
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/614,935
 ; FILING DATE: 11-MAR-1996
 ; CLASSIFICATION: 436
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Jackson Esq., David A.
 ; REGISTRATION NUMBER: 26,742
 ; REFERENCE/DOCKET NUMBER: 600-1-156
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 201-487-5800
 ; TELEFAX: 201-343-1684
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 204 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; HYPOTHETICAL: NO
 ; ANTI-SENSE: NO
 ; FRAGMENT TYPE:
 ; ORIGINAL SOURCE:
 ; ORGANISM: Vespula vulgaris
 ; US-08-614-935-2

Query Match 100.0%; Score 220; DB 1; Length 204;
 Best Local Similarity 100.0%; Pred. No. 2e-21;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCNGKVKVVSGLTKQ 39
 Db 1 NNYCKIKLKGCVHTACKYGLKPCNGKVKVVSGLTKQ 39

RESULT 3
 US-09-130-287-2
 ; Sequence 2, Application US/09130287
 ; Patent No. 6106844
 ; GENERAL INFORMATION:
 ; APPLICANT: King, Te P.
 ; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
 ; NUMBER OF SEQUENCES: 81
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: David A. Jackson, Esq.

STREET: 411 Hackensack Ave, Continental Plaza, 4th
 STREET: Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/130,287
 FILING DATE: 2000-04-03
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/614,935
 FILING DATE: 11-MAR-1996
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-156 DIV
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 2:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 204 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE:
 ORIGINAL SOURCE:
 ORGANISM: Vespula vulgaris
 US-09-130-287-2

Query Match 100.0%; Score 220; DB 2; Length 204;
 Best Local Similarity 100.0%; Pred. No. 2e-21;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCNGKVKVVSGLTKQ 39
 Db 1 NNYCKIKLKGCVHTACKYGLKPCNGKVKVVSGLTKQ 39

RESULT 4
 US-09-541-759-6
 ; Sequence 6, Application US/09541759
 ; Patent No. 6723322
 ; GENERAL INFORMATION:
 ; APPLICANT: Lustigman, Sara
 ; APPLICANT: Pearlman, Eric
 ; APPLICANT: Unnasch, Thomas
 ; TITLE OF INVENTION: ANGIOGENIC ONCHOCERCA VOLVULUS PROTEINS AND USES THEREOF
 ; FILE REFERENCE: 63475/252
 ; CURRENT APPLICATION NUMBER: US/09/541,759
 ; CURRENT FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: Patent in version 3.0
 ; SEQ ID NO 6
 ; LENGTH: 227
 ; TYPE: PRT
 ; ORGANISM: Vespula vulgaris
 ; US-09-541-759-6

Query Match 100.0%; Score 220; DB 2; Length 227;
 Best Local Similarity 100.0%; Pred. No. 2.3e-21;
 Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:57:41 ; Search time 11.7595 Seconds
(without alignments)
274.190 Million cell updates/sec

Title: US-10-091-135-5
Perfect score: 220
Sequence: 1 NNYCKIKLGGVHTACKYGSILKPNCGNKVNVVYGLTKQ 39

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA: *
1: /cgn2_6/ptodata/1/1aa/5 COMB.pep.*
2: /cgn2_6/ptodata/1/1aa/6 COMB.pep.*
3: /cgn2_6/ptodata/1/1aa/H COMB.pep.*
4: /cgn2_6/ptodata/1/1aa/PCTUS COMB.pep.*
5: /cgn2_6/ptodata/1/1aa/RE COMB.pep.*
6: /cgn2_6/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	220	100.0	204	1	US-08-419-414-9 Sequence 9, Appli
2	220	100.0	204	1	US-08-614-935-2 Sequence 2, Appli
3	220	100.0	204	2	US-09-130-287-2 Sequence 2, Appli
4	220	100.0	227	2	US-09-541-759-6 Sequence 6, Appli
5	214	97.3	204	1	US-08-614-935-1 Sequence 1, Appli
6	214	97.3	204	2	US-09-130-287-1 Sequence 1, Appli
7	180	81.8	31	1	US-08-614-935-46 Sequence 46, Appli
8	180	81.8	31	2	US-09-130-287-46 Sequence 46, Appli
9	174	79.1	31	1	US-08-614-935-45 Sequence 45, Appli
10	174	79.1	31	2	US-09-130-287-45 Sequence 45, Appli
11	145	65.9	204	1	US-08-614-935-5 Sequence 5, Appli
12	145	65.9	204	2	US-09-130-287-5 Sequence 5, Appli
13	133.5	60.7	203	1	US-08-419-414-8 Sequence 8, Appli
14	133.5	60.7	203	1	US-08-614-935-3 Sequence 3, Appli
15	133.5	60.7	203	2	US-09-130-287-3 Sequence 3, Appli
16	132	60.0	205	1	US-08-614-935-4 Sequence 4, Appli
17	132	60.0	205	2	US-09-130-287-4 Sequence 4, Appli
18	126	57.3	32	1	US-08-614-935-48 Sequence 48, Appli
19	126	57.3	32	2	US-09-130-287-48 Sequence 48, Appli
20	124	56.4	32	1	US-08-614-935-49 Sequence 49, Appli
21	124	56.4	32	2	US-09-130-287-49 Sequence 49, Appli
22	119	54.1	32	1	US-08-614-935-42 Sequence 42, Appli
23	119	54.1	32	2	US-09-130-287-42 Sequence 42, Appli
24	112.5	51.1	31	1	US-08-614-935-47 Sequence 47, Appli
25	112.5	51.1	31	2	US-09-130-287-47 Sequence 47, Appli
26	106	48.2	205	1	US-08-419-414-10 Sequence 10, Appli
27	106	48.2	205	1	US-08-614-935-6 Sequence 6, Appli

28	106	48.2	205	1	US-08-614-935-7 Sequence 7, Appli
29	106	48.2	205	2	US-09-130-287-6 Sequence 6, Appli
30	106	48.2	205	2	US-09-130-287-7 Sequence 7, Appli
31	94	42.7	34	1	US-08-614-935-50 Sequence 50, Appli
32	94	42.7	34	1	US-08-614-935-51 Sequence 51, Appli
33	94	42.7	34	2	US-09-130-287-50 Sequence 50, Appli
34	94	42.7	34	2	US-09-130-287-51 Sequence 51, Appli
35	88.5	40.2	20	1	US-08-614-935-8 Sequence 8, Appli
36	88.5	40.2	20	2	US-09-130-287-8 Sequence 8, Appli
37	76.5	34.8	20	1	US-08-614-935-9 Sequence 9, Appli
38	76.5	34.8	20	2	US-09-130-287-9 Sequence 9, Appli
39	72.5	33.0	34	1	US-08-614-935-33 Sequence 33, Appli
40	72.5	33.0	34	2	US-09-130-287-33 Sequence 33, Appli
41	68	30.9	20	1	US-08-614-935-10 Sequence 10, Appli
42	68	30.9	20	2	US-09-130-287-10 Sequence 10, Appli
43	65.5	29.8	1935	2	US-09-949-016-10403 Sequence 10403, A
44	65.5	29.8	2871	2	US-09-538-092-1076 Sequence 1076, Ap
45	64	29.1	20	1	US-08-614-935-31 Sequence 31, Appli

ALIGNMENTS

RESULT 1
US-08-419-414-9
; Sequence 9, Application US/08419414
; Patent No. 5753787
; GENERAL INFORMATION:
; APPLICANT: Hawdon, John M.
; APPLICANT: Hotez, Peter J.
; APPLICANT: Jones, Brian F.
; TITLE OF INVENTION: Hookworm Vaccine
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patrea L. Pabat
; STREET: 2800 One Atlantic Center
; STREET: 1201 West Peachtree Street
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/419,414
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabat, Patrea L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: YU113
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) 873-8795
; TELEFAX: (404) 873-8795
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 204 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Vespula vulgaris
; US-08-419-414-9

Query Match 100.0%; Score 220; DB 1; Length 204;
Best Local Similarity 100.0%; Pred. No. 2e-21;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Best Local Similarity 100.0%; Pred. No. 5.6e-21;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCGKGVVSYGLTKQ 39
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DB 1 NNYCKIKLKGCVHTACKYGLKPCGKGVVSYGLTKQ 39

RESULT 2

VAS_VESVU STANDARD; PRT; 227 AA.
ID VAS_VESVU
AC Q05110; Q9UB91;
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE venom allergen 5 precursor (Antigen 5) (Ag5) (Allergen Ves v 5) (Ves v V).
DE Vesputia vulgaris (Yellow jacket) (Wasp).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
OC NCBI_TaxID=7454;

RN NUCLEOTIDE SEQUENCE, AND PARTIAL PROTEIN SEQUENCE.

RC TISSUE=Venom;
RX MEDLINE=93203603; PubMed=8454859;
RA Lu G., Villalba M., Coscia M.R., Hoffman D.R., King T.P.;
RT "Sequence analysis and antigenic cross-reactivity of a venom allergen,
antigen 5, from hornets, wasps, and yellow jackets.";
J. Immunol. 150:2823-2830(1993).
(2)

RN NUCLEOTIDE SEQUENCE OF 24-227.

RA Suck R., Hagen S., Fiebig H.;
RT "Molecular cloning of a genomic sequence from the venom allergen
antigen 5 from Vesputia vulgaris.";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
CC -1- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -1- ALLEGEN: Causes an allergic reaction in human.
CC -1- SIMILARITY: Belongs to the CRISP family.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

CC EMBL; M98858; AAA30333.1; -; mRNA.
CC EMBL; AJ238849; CAB42887.1; -; Genomic DNA.

DR PDB; 1QNX; X-ray; A=24-227.

DR InterPro; IPR001283; Allrgn_V5/Tpx1.

DR InterPro; IPR002413; V5_allergen.

DR Pfam; PF00188; SCP; 1.

DR PRINTS; PR00838; VSALLERGEN.

DR PRINTS; PR00837; V5TPXLIKE.

DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.

DR SMART; SM00198; SCP; 1.

DR PROSITE; PS01009; CRISP_1; 1.

DR PROSITE; PS01010; CRISP_2; 1.

KW 3D-structure; Allergen; Direct protein sequencing; Signal.

FT SIGNAL 1 23

FT CHAIN 24 227 Venom allergen 5.

FT DISULFID 27 40 By similarity.

FT DISULFID 31 124 By similarity.

FT DISULFID 49 117 By similarity.

FT DISULFID 193 210 V -> I (in Ref. 2).

FT CONFLICT 109 109 O -> E (in Ref. 2).

FT CONFLICT 118 118 D -> N (in Ref. 2).

FT CONFLICT 173 173 M -> K (in Ref. 2).

FT CONFLICT 219 219

FT HELIX 26 28

FT TURN 32 33

FT HELIX 38 41

FT STRAND 53 57

FT HELIX 61 79
FT TURN 80 81
FT TURN 87 88
FT STRAND 94 94
FT STRAND 101 102
FT HELIX 104 114
FT TURN 115 116
FT STRAND 133 141
FT HELIX 149 157
FT HELIX 158 162
FT TURN 165 166
FT HELIX 169 171
FT HELIX 174 183
FT TURN 184 184
FT TURN 186 187
FT STRAND 190 200
FT TURN 201 202
FT STRAND 203 213
FT TURN 219 220
FT STRAND 226 227
SQ SEQUENCE 227 AA; 25798 MW; 99E9813740A66F55 CRC64;

Query Match 100.0%; Score 220; DB 1; Length 227;

Best Local Similarity 100.0%; Pred. No. 6.3e-21;

Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGLKPCGKGVVSYGLTKQ 39

|||||

DB 24 NNYCKIKLKGCVHTACKYGLKPCGKGVVSYGLTKQ 62

RESULT 3

VAS_VESPE STANDARD; PRT; 204 AA.

ID VAS_VESPE

AC P35785;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves p 5) (Ves p V).

OS Vesputia pensylvanica (Western yellow jacket) (Wasp).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;

OC Vespidae; Vespinae; Vespula.

OC NCBI_TaxID=30213;

RN [1]

RP PROTEIN SEQUENCE.

RC TISSUE=Venom;

RX MEDLINE=94044316; PubMed=8227862;

RA Hoffman D.R.;

RT "Allergens in Hymenoptera venom. XXV: the amino acid sequences of

antigen 5 molecules and the structural basis of antigenic cross-

reactivity.";

RL J. Allergy Clin. Immunol. 92:707-716(1993).

CC -1- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.

CC -1- ALLEGEN: Causes an allergic reaction in human.

CC -1- SIMILARITY: Belongs to the CRISP family.

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between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

CC PIR; C44583; C44583.

DR HSPG; Q05110; 1QNX.

DR SMK; P35785; 1-204.

DR InterPro; IPR001283; Allrgn_V5/Tpx1.

DR InterPro; IPR002413; V5_allergen.

DR Pfam; PF00188; SCP; 1.

DR PRINTS; PR00838; VSALLERGEN.

DR PRINTS; PR00837; V5TPXLIKE.

DR ProDom; PD000542; Allrgn_V5/Tpx1; 1.

DR SMART; SM00198; SCP; 1.

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: April 18, 2006, 10:53:37 ; Search time 57.6069 Seconds
(without alignments)
477.644 Million cell updates/sec

Title: US-10-091-135-5

Perfect score: 220

Sequence: 1 NNYCKIKLKGCVHTACKYGLKPNCGNKVVSGLTKQ 39

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Uniprot_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	220	100.0	204	1 VAS_VESFL	P35783 vespula fla
2	220	100.0	227	1 VAS_VESFU	Q05110 vespula vul
3	216	98.2	204	1 VAS_VESPE	P35785 vespula pen
4	214	97.3	204	1 VAS_VESNC	P35760 vespula mac
5	197	89.5	204	1 VAS_VESGE	P35784 vespula ger
6	169.5	77.0	205	1 VAS_VESQ	P35786 vespula squ
7	168.5	76.6	206	1 VAS_VESVI	P35787 vespula vid
8	146	66.4	202	1 VAS1_VESCR	P35781 vespula crabr
9	146	66.4	202	1 VAS2_VESCR	P35782 vespula crabr
10	145	65.9	227	1 VAS2_DOLMA	P10736 dolichovesp
11	137	62.3	202	1 VAS_VESMA	P81657 vespula manda
12	133.5	60.7	203	1 VAS_DOLAR	Q05108 dolichovesp
13	130	59.1	215	1 VAS3_DOLMA	P10737 dolichovesp
14	114	51.8	206	1 VAS_FOLGA	P83177 polistes ga
15	111	50.5	206	1 VAS_FOLDJO	P81656 polistes do
16	111	50.5	227	2 Q68KJ8_POLDO	Q68KJ8 polistes do
17	108	49.1	205	1 VAS_POLFU	P35780 polistes fu
18	106	48.2	205	1 VAS_POLEX	P35759 polistes ex
19	106	48.2	209	1 VAS_POLAN	Q05109 polistes ex
20	103	46.8	226	2 Q68KJ9_POLEX	Q68KJ9 polistes ex
21	90.5	41.1	207	1 VAS_POLSR	Q72156 polybia scu
22	67.5	30.7	2884	2 Q4SHN1_TETNG	Q4SHN1 tetraodon n
23	65.5	29.8	195	2 Q75N89_HUMAN	Q75N89 homo sapien
24	65.5	29.8	1095	2 Q60784_MOUSE	Q60784 mus musculu
25	65.5	29.8	1365	2 Q75N88_HUMAN	Q75N88 homo sapien
26	65.5	29.8	2871	1 FBNI_BOVIN	P98133 bos taurus
27	65.5	29.8	2871	1 FBNI_HUMAN	P35555 homo sapien
28	65.5	29.8	2871	1 FBNI_MOUSE	Q61554 mus musculu
29	65.5	29.8	2871	1 FBNI_PIG	Q9TV36 sus scrofa
30	65.5	29.8	2871	2 Q75N87_HUMAN	Q75N87 homo sapien
31	65.5	29.8	2872	2 Q9WUH8_RAT	Q9WUH8 rattus norv

32	65.5	29.8	3857	2	Q88840_MOUSE	Q88840 mus musculu
33	64.5	29.3	610	2	Q54FR6_DICDI	Q54FR6 dictyosteli
34	63.5	28.9	135	2	Q6S964_PLAFA	Q6S964 plasmodium
35	61	27.7	70	2	Q4SX80_TETNG	Q4SX80 tetraodon n
36	61	27.7	1295	1	GLP1_CAEEL	P13508 caenorhabdi
37	61	27.7	2025	2	Q9SHK4_ARATH	Q9SHK4 arabidopsis
38	60.5	27.5	350	2	Q813D6_PLAFA7	Q813D6 plasmodium
39	60	27.3	396	2	Q5FUF4_GLUOX	Q5FUF4 gluconobact
40	59.5	27.0	311	2	Q5SLJ6_CRYNE	Q5SLJ6 cryptococcu
41	59.5	27.0	311	2	Q5KDJ6_CRYNE	Q5KDJ6 cryptococcu
42	59.5	27.0	315	2	Q55PN7_CRYNE	Q55PN7 cryptococcu
43	59.5	27.0	359	2	Q5KDR9_CRYNE	Q5KDR9 cryptococcu
44	59.5	27.0	542	1	V155_FOWPV	Q9JSA7 fowlpox vir
45	59	26.8	113	2	Q4QQ77_DROME	Q4QQ77 drosophila

ALIGNMENTS

RESULT 1
ID VAS_VESFL STANDARD; PRT; 204 AA.
AC P35783;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DE 05-JUL-2004 (Rel. 44, Last annotation update)
DE Venom allergen 5 (Antigen 5) (Ag5) (Allergen Ves f 5) (Ves f V).
OS Vespula flavopilosa (Yellow jacket) (Wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespula.
OX NCBI_TaxId=30211;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=94044316; PubMed=8227862;
RA Hoffman D.R.;
RT "Allergens in Hymenoptera venom. XXV: the amino acid sequences of
RT antigen 5 molecules and the structural basis of antigenic cross-
RT reactivity.";
RL J. Allergy Clin. Immunol. 92:707-716(1993).
CC -!- FUNCTION: May have an ancestral function in the promotion of ovum
CC fertilization by sperm.
CC -!- SUBCELLULAR LOCATION: Secreted; wasp venom reservoirs.
CC -!- ALLERGEN: Causes an allergic reaction in human.
CC -!- SIMILARITY: Belongs to the CRISP family.

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between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

PIR; A44583; A44583.
HSSP; Q05110; 1QNK.
SMR; P35783; 1-204.
InterPro; IPR001283; Allrgn_V5/Tpx1.
InterPro; IPR002413; V5_allergen.
Pfam; PF00188; SCP; 1.
PRINTS; PR00838; V5ALLERGEN.
PRINTS; PR00837; V5TPXLIKE.
ProDom; PD000542; Allrgn_V5/Tpx1; 1.
SMART; SM00198; SCP; 1.
PROSITE; PS01009; CRISP_1; 1.
PROSITE; PS01010; CRISP_2; 1.
Allergen; Direct protein sequencing.
FT DISULFID 4 17 By similarity.
FT DISULFID 8 101 By similarity.
FT DISULFID 26 94 By similarity.
FT DISULFID 170 187 By similarity.
SQ SEQUENCE 204 AA; 23274 MW; 7667232536AB2FC5 CRC64;
Query Match 100.0%; Score 220; DB 1; Length 204;

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RESULT 3
B37329
antigen 5 - eastern yellowjacket
C;Species: Vespula maculifrons (eastern yellowjacket)
C;Date: 06-Nov-1992 #sequence_revision 06-Nov-1992 #text_change 09-Jul-2004
C;Accession: B37329
R;Lu, G.; Villalba, M.; Coscia, M.R.; Hoffman, D.R.; King, T.P.
submitted to the Protein Sequence Database, August 1992
A;Reference number: A37329
A;Accession: B37329
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-204 <HOF>
A;Cross-references: UNIPROT:P35760; UNIPARC:UPI0000138092
C;Superfamily: yellowjacket venom allergen antigen 5

Query Match          97.3%; Score 214; DB 2; Length 204;
Best Local Similarity 97.4%; Pred. No. 1.8e-19;
Matches 38; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGSLLKPNCGNKVWVSYGLTKQ 39
DB 1 NNYCKIKLKGCVHTACKYGSLLKPNCGNKVWVSYGLTKQ 39

RESULT 4
B44583
venom allergen antigen Ves g 5 - German yellowjacket
C;Species: Vespula germanica (German yellowjacket)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: B44583; A44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5
A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: B44583
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-204 <HOF>
A;Cross-references: UNIPROT:P35784; UNIPARC:UPI0000138090
C;Superfamily: yellowjacket venom allergen antigen 5

Query Match          89.5%; Score 197; DB 2; Length 204;
Best Local Similarity 89.7%; Pred. No. 2.5e-17;
Matches 35; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 NNYCKIKLKGCVHTACKYGSLLKPNCGNKVWVSYGLTKQ 39
DB 1 NNYCKIKLKGCVHTACKYGSLLKPNCGNKVWVSYGLTKQ 39

RESULT 5
D44583
venom allergen antigen Ves s 5 - southern yellowjacket
C;Species: Vespula squamosa (southern yellowjacket)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: D44583; D44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5
A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: D44583
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-205 <HOF>
A;Cross-references: UNIPROT:P35786; UNIPARC:UPI0000138094
C;Superfamily: yellowjacket venom allergen antigen 5

Query Match          77.0%; Score 169.5; DB 2; Length 205;
Best Local Similarity 81.6%; Pred. No. 6.8e-14;
Matches 31; Conservative 3; Mismatches 3; Indels 1; Gaps 1;

QY 2 NYCKIKLKGCVHTACKYGSLLKPNCGNKVWVSYGLTK 38
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DB 2 DYCKIKLKGCVHTACKYGTSTKPNCGNKVWVSYGVTO 39

RESULT 6
E44583
venom allergen antigen Ves vi 5 - yellowjacket (Vespula vidua)
C;Species: Vespula vidua
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: E44583; E44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5
A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: E44583
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-206 <HOF>
A;Cross-references: UNIPROT:P35787; UNIPARC:UPI0000138095
C;Superfamily: yellowjacket venom allergen antigen 5

Query Match          76.6%; Score 168.5; DB 2; Length 206;
Best Local Similarity 81.6%; Pred. No. 9.1e-14;
Matches 31; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 2 NYCKIKLKGCVHTACKYGSLLKPNCGNKVWVSYGLTK 38
DB 3 NYCKIKLKGCVHTACKYGTSTKPNCGNKVWVSYGLTE 40

RESULT 7
H44583
venom allergen antigen Vesp c 5.02 - European hornet
C;Species: Vespa crabro (European hornet)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: H44583; H44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5
A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: H44583
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-202 <HOF>
A;Cross-references: UNIPROT:P35782; UNIPARC:UPI0000138080
C;Superfamily: yellowjacket venom allergen antigen 5

Query Match          66.4%; Score 146; DB 2; Length 202;
Best Local Similarity 70.0%; Pred. No. 5.8e-11;
Matches 28; Conservative 3; Mismatches 7; Indels 2; Gaps 2;

QY 1 NNYCKIKLKGCVHTACKYGSLLKPNCGNKVWVSYGLTKQ 39
DB 1 NNYCKIKC-RSGIHTLCKYGTSTKPNCGNKVWVSYGLTKQ 39

RESULT 8
G44583
venom allergen antigen Vesp c 5.01 - European hornet
C;Species: Vespa crabro (European hornet)
C;Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C;Accession: G44583; G44522
R;Hoffman, D.R.
J. Allergy Clin. Immunol. 92, 707-716, 1993
A;Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5
A;Reference number: A44583; MUID:94044316; PMID:8227862
A;Accession: G44583
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-202 <HOF>
A;Cross-references: UNIPROT:P35781; UNIPARC:UPI000013807C
C;Superfamily: yellowjacket venom allergen antigen 5
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:56:21 ; Search time 8.18702 Seconds
(without alignments)
458.342 Million cell updates/sec

Title: US-10-091-135-5

Perfect score: 220

Sequence: 1 NNYCKIKLKGCVHTACKYGLKPCNCGNKVVSYGLTKQ 39

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR_80:*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	220	100.0	204	2 A44583	venom allergen ant
2	216	98.2	204	2 C44583	venom allergen ant
3	214	97.3	204	2 B37329	antigen 5 - easter
4	197	89.5	204	2 B44583	venom allergen ant
5	169.5	77.0	205	2 D44583	venom allergen ant
6	168.5	76.6	206	2 E44583	venom allergen ant
7	146	66.4	202	2 H44583	venom allergen ant
8	146	66.4	202	2 G44583	venom allergen ant
9	145	65.9	227	2 A31085	antigen 5-2 precu
10	132	60.0	213	2 B31085	antigen 5-3 precu
11	108	49.1	205	2 F44583	venom allergen ant
12	106	48.2	205	2 A37329	antigen 5 - paper
13	65.5	29.8	2871	2 A5567	fibrillin I - bovi
14	65.5	29.8	2871	2 A5567	fibrillin-1 precu
15	65.5	29.8	3002	2 A47221	fibrillin-1 precu
16	61	27.7	1295	2 A32901	glp1 protein precu
17	61	27.7	1295	2 D86201	protein F12K11.6 [
18	58.5	26.6	258	2 A33953	enterotoxin D prec
19	58.5	26.6	401	2 G96972	hypothetical prote
20	58.5	26.6	1469	2 T19459	hypothetical prote
21	58.5	26.6	2907	2 A57278	fibrillin-2 precu
22	58	26.4	1712	2 A38261	masking protein pr
23	58	26.4	2918	2 A54105	fibrillin-2 precu
24	56.5	25.7	292	2 H81857	hypothetical prote
25	56.5	25.7	342	2 B81086	hypothetical prote
26	56	25.5	2496	2 A71616	secreted protein P
27	54	24.5	211	2 B58853	venom allergen sol
28	54	24.5	212	2 B37330	venom allergen iii
29	54	24.5	251	2 A55035	cysteine-rich prot

30	53	24.1	362	2 I40304	outer membrane lip
31	53	24.1	453	1 A25326	acid phosphatase (
32	53	24.1	4910	2 S64942	probable membrane
33	52.5	23.9	730	2 B85013	hypothetical prote
34	52.5	23.9	730	2 T10539	hypothetical prote
35	52	23.6	79	2 T07917	antifungal protein
36	52	23.6	79	2 T10243	antifungal protein
37	52	23.6	87	2 T00564	gibberellin-regula
38	52	23.6	95	2 H72271	ferredoxin - Therm
39	52	23.6	143	2 C97970	hypothetical prote
40	52	23.6	1975	2 B81192	hemagglutinin/hemo
41	52	23.6	1995	2 G81044	hemagglutinin/hemo
42	51.5	23.4	341	2 T05764	hypothetical prote
43	51.5	23.4	1294	2 S77690	probable membrane
44	51	23.2	80	2 T10183	antifungal protein
45	50.5	23.0	260	2 B89969	enterotoxin Seo [i

ALIGNMENTS

RESULT 1

A44583
venom allergen antigen Ves f 5 - yellowjacket (Vespula flavopilosa)
C:Species: Vespula flavopilosa
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: A44583; B44522
R:Hoffman, D.R.

J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mol.
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: A44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>

A:Cross-references: UNIPROT:P35783; UNIPARC:UPI000013808F
C:Superfamily: yellowjacket venom allergen antigen 5
Query Match 100.0%; Score 220; DB 2; Length 204;
Best Local Similarity 100.0%; Pred. No. 3.3e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCNCGNKVVSYGLTKQ 39
Db 1 NNYCKIKLKGCVHTACKYGLKPCNCGNKVVSYGLTKQ 39

RESULT 2

C44583
venom allergen antigen Ves p 5 - western yellowjacket
C:Species: Vespula pensylvanica (western yellowjacket)
C:Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
C:Accession: C44583; C44522
R:Hoffman, D.R.

J. Allergy Clin. Immunol. 92, 707-716, 1993
A:Title: Allergens in hymenoptera venom XXV: the amino acid sequences of antigen 5 mol.
A:Reference number: A44583; MUID:94044316; PMID:8227862
A:Accession: C44583
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-204 <HOF>

A:Cross-references: UNIPROT:P35785; UNIPARC:UPI0000138093
C:Superfamily: yellowjacket venom allergen antigen 5
Query Match 98.2%; Score 216; DB 2; Length 204;
Best Local Similarity 94.9%; Pred. No. 1e-19;
Matches 37; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NNYCKIKLKGCVHTACKYGLKPCNCGNKVVSYGLTKQ 39
Db 1 NNYCKIKLKGCVHTACKYGLKPCNCGNKVVSYGLTKE 39

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XX SQ Sequence 39 AA;
Query Match 100.0%; Score 220; DB 5; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NNYCKIKCLKGGVHTACKYGLKPNCGNKVWVSYGLTKQ 39
|||||
Db 1 NNYCKIKCLKGGVHTACKYGLKPNCGNKVWVSYGLTKQ 39

RESULT 2
AAE28812
ID AAE28812 standard; peptide; 46 AA.
XX
AC AAE28812;
XX
DT 27-DEC-2002 (first entry)
XX
DE Vespula vulgaris antigen 5 (Ves V5) allergen peptide #6.
XX
KW Allergen; hybrid protein; allergenicity; immune system related disease;
KW immunogenicity; allergy; vaccine; antigen 5.
XX
OS Vespula vulgaris.
XX
PN WO200270665-A2.
XX
PD 12-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006765.
XX
PR 02-MAR-2001; 2001US-0272818P.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
PA (ALKA-) ALK-ABELLO AS.
XX
PI King TP, Spangfort MD;
XX
WPI; 2002-698751/75.
DR N-PSDB; AAD46230.
XX
PT New allergen hybrid protein having reduced allergenicity but retaining
PT immunogenicity, useful for treating allergy or immune system related
PT diseases.
XX
PS Claim 17; Page 151; 222pp; English.
XX
CC The present invention relates to recombinant allergen hybrid proteins
CC having reduced allergenicity but retaining immunogenicity. The hybrid
CC proteins comprise a peptide epitope sequence of an allergen protein and a
CC scaffold protein that is structurally homologous to the allergen protein.
CC Sequences of the invention comprise a native conformation and the peptide
CC epitope sequence is present in a surface accessible region of the hybrid
CC protein corresponding to its position in the allergen protein. The hybrid
CC proteins are useful for treating allergy or immune system related
CC diseases. They are also used as vaccines. The present sequence is Vespula
CC vulgaris antigen 5 (Ves V5) allergen peptide
XX
SQ Sequence 46 AA;
Query Match 100.0%; Score 220; DB 5; Length 46;
Best Local Similarity 100.0%; Pred. No. 1.5e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NNYCKIKCLKGGVHTACKYGLKPNCGNKVWVSYGLTKQ 39
|||||
Db 1 NNYCKIKCLKGGVHTACKYGLKPNCGNKVWVSYGLTKQ 39

RESULT 3
AAE28827
ID AAE28827 standard; peptide; 50 AA.
XX
AC AAE28827;
XX
DT 27-DEC-2002 (first entry)
XX
DE Vespula vulgaris antigen 5 (Ves V5) allergen peptide #14.
XX
KW Allergen; hybrid protein; allergenicity; immune system related disease;
KW immunogenicity; allergy; vaccine; antigen 5.
XX
OS Vespula vulgaris.
XX
PN WO200270665-A2.
XX
PD 12-SEP-2002.
XX
PF 04-MAR-2002; 2002WO-US006765.
XX
PR 02-MAR-2001; 2001US-0272818P.
XX
PA (UYRQ ) UNIV ROCKEFELLER.
PA (ALKA-) ALK-ABELLO AS.
XX
PI King TP, Spangfort MD;
XX
WPI; 2002-698751/75.
DR N-PSDB; AAD46272.
XX
PT New allergen hybrid protein having reduced allergenicity but retaining
PT immunogenicity, useful for treating allergy or immune system related
PT diseases.
XX
PS Claim 17; Page 152; 222pp; English.
XX
CC The present invention relates to recombinant allergen hybrid proteins
CC having reduced allergenicity but retaining immunogenicity. The hybrid
CC proteins comprise a peptide epitope sequence of an allergen protein and a
CC scaffold protein that is structurally homologous to the allergen protein.
CC Sequences of the invention comprise a native conformation and the peptide
CC epitope sequence is present in a surface accessible region of the hybrid
CC protein corresponding to its position in the allergen protein. The hybrid
CC proteins are useful for treating allergy or immune system related
CC diseases. They are also used as vaccines. The present sequence is Vespula
CC vulgaris antigen 5 (Ves V5) allergen peptide
XX
SQ Sequence 50 AA;
Query Match 100.0%; Score 220; DB 5; Length 50;
Best Local Similarity 100.0%; Pred. No. 1.6e-20;
Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 NNYCKIKCLKGGVHTACKYGLKPNCGNKVWVSYGLTKQ 39
|||||
Db 1 NNYCKIKCLKGGVHTACKYGLKPNCGNKVWVSYGLTKQ 39

RESULT 4
AAE28828
ID AAE28828 standard; peptide; 57 AA.
XX
AC AAE28828;
XX
DT 27-DEC-2002 (first entry)
XX
DE Vespula vulgaris antigen 5 (Ves V5) allergen peptide #15.
XX
KW Allergen; hybrid protein; allergenicity; immune system related disease;
KW immunogenicity; allergy; vaccine; antigen 5.
XX
OS Vespula vulgaris.
XX
PN WO200270665-A2.
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 18, 2006, 10:52:17 ; Search time 54.3321 Seconds
(without alignments)
315.390 Million cell updates/sec

Title: US-10-091-135-5

Perfect score: 220

Sequence: 1 NNYCKIKLGKGVHTACKYKSLKPCNGKVVVSYGLTKQ 39

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 21.*

- 1: geneseqp1980s.*
- 2: geneseqp1990s.*
- 3: geneseqp2000s.*
- 4: geneseqp2001s.*
- 5: geneseqp2002s.*
- 6: geneseqp2003as.*
- 7: geneseqp2003bs.*
- 8: geneseqp2004s.*
- 9: geneseqp2005s.*

.Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	220	100.0	39	AAE28811	Aae28811 Vespula v
2	220	100.0	46	AAE28812	Aae28812 Vespula v
3	220	100.0	50	AAE28827	Aae28827 Vespula v
4	220	100.0	57	AAE28828	Aae28828 Vespula v
5	220	100.0	76	AAE28829	Aae28829 Vespula v
6	220	100.0	204	AAW35688	Aaw35688 Vespul an
7	220	100.0	204	AAW45217	Aay45217 Wild type
8	220	100.0	204	ABG66983	Abg66983 Wasp veno
9	220	100.0	204	ABG67052	Abg67052 Wasp veno
10	220	100.0	204	ABG67104	Abg67104 Wasp veno
11	220	100.0	204	ABG67103	Abg67103 Wasp veno
12	220	100.0	204	AAE28820	Aae28820 Vespula v
13	220	100.0	209	ABM00031	Abm00031 Allergen
14	220	100.0	227	AAW25644	Aay25644 Vespula s
15	220	100.0	227	AAE13071	Aae13071 Vespula v
16	220	100.0	227	ADC34893	Adc34893 Wasp alle
17	214	97.3	204	AAW35687	Aaw35687 Vespul an
18	214	97.3	204	ABG66977	Abg66977 Wasp veno
19	184	83.6	32	AAE28810	Aae28810 Vespula v
20	180	81.8	31	AAW35648	Aaw35648 t cell pe
21	174	79.1	31	AAW35647	Aaw35647 t cell pe
22	168.5	76.6	206	AAW25648	Aay25648 Vespula s
23	168.5	76.6	206	ADC34897	Adc34897 Wasp alle
24	145	65.9	204	AAW35691	Aaw35691 Vespul an

25	140	63.6	24	5	AAE28809	Aae28809 Vespula v
26	133.5	60.7	203	2	AAW35689	Aaw35689 Vespul an
27	132	60.0	205	2	AAW35690	Aaw35690 Vespul an
28	126	57.3	32	2	AAW35650	Aaw35650 T cell pe
29	124	56.4	32	2	AAW35651	Aaw35651 T cell pe
30	119	54.1	32	2	AAW35644	Aaw35644 Immunomod
31	112.5	51.1	31	2	AAW35649	Aaw35649 T cell pe
32	107	48.6	18	5	AAE28808	Aae28808 Vespula v
33	106	48.2	205	2	AAW35693	Aaw35693 Vespul an
34	106	48.2	205	2	AAW35692	Aaw35692 Vespul an
35	106	48.2	205	5	AAE28821	Aae28821 Pollistes
36	94	42.7	34	2	AAW35652	Aaw35652 T cell pe
37	94	42.7	34	2	AAW35653	Aaw35653 T cell pe
38	88.5	40.2	20	2	AAW35635	Aaw35635 Immunomod
39	79.5	36.1	34	2	AAW35620	Aaw35620 Immunomod
40	76.5	34.8	20	2	AAW35633	Aaw35633 Immunomod
41	71	32.3	20	2	AAW35694	Aaw35694 D. macula
42	68	30.9	20	2	AAW35694	Abm81619 Tumour-as
43	65.5	29.8	2871	8	ABM81619	Abm81619 Tumour-as
44	65.5	29.8	2871	9	ADX05916	Adx05916 Cyclin-de
45	65.5	29.8	2871	9	ADZ70705	Adz70705 Human pro

ALIGNMENTS

RESULT 1
AAE28811
ID AAE28811 standard; peptide; 39 AA.
XX
AC AAE28811;
XX
DT 27-DEC-2002 (first entry)
XX

DE Vespula vulgaris antigen 5 (Ves V5) allergen peptide #5.

XX Allergen; hybrid protein; allergenicity; immune system related disease;
KW immunogenicity; allergy; vaccine; antigen 5.
XX

OS Vespula vulgaris.

XX WO200270665-A2.

XX 12-SEP-2002.

XX 04-MAR-2002; 2002WO-US006765.

XX 02-MAR-2001; 2001US-0272818P.

XX (UYRQ) UNIV ROCKEFELLER.
(ALKA-) ALK-ABELLO AS.

XX King TP, Spangfort MD;

XX WPI; 2002-698751/75.

XX N-PSDB; AAD46229.

XX New allergen hybrid protein having reduced allergenicity but retaining immunogenicity, useful for treating allergy or immune system related diseases.

XX Claim 17; Page 151; 222pp; English.

XX The present invention relates to recombinant allergen hybrid proteins having reduced allergenicity but retaining immunogenicity. The hybrid proteins comprise a peptide epitope sequence of an allergen protein and a scaffold protein that is structurally homologous to the allergen protein. Sequences of the invention comprise a native conformation and the hybrid epitope sequence is present in a surface accessible region of the hybrid protein corresponding to its position in the allergen protein. The hybrid proteins are useful for treating allergy or immune system related diseases. They are also used as vaccines. The present sequence is Vespula vulgaris antigen 5 (Ves V5) allergen peptide